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961.954 Million cell updates/sec
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2: uniprot_trembl:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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MRGD MOUSE
BAD20640
MRGD RAT
BAD20639
    MRG4_HUMAN
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SNS3_HUMAN
SNS3_HUMAN
MRG1_HUMAN
MRG2_HUMAN
AAH63450
SNS1_RAT
Q8CLP3
Q7IN45
Q912C0
AAH67292
MGA3_MOUSE
MRG3_HUMAN
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Bad20639 rattus no
O961a9 homo sapien
O8tdd7 homo sapien
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O7tn42 rattus norv
O961b1 homo sapien
O7tn42 rattus norv
O961b3 mus musculu
O7tn45 rattus norv
O91w03 mus musculu
O7tn46 rattus norv
O91w03 mus musculu
O7tn49 rattus norv
O91w04 mus musculu
O961b0 homo sapien
O91ww2 mus musculu
O961b0 rattus norv
O91w04 mus musculu
O71c148 rattus norv
O91zc4 mis musculu
O71c148 rattus norv
O8tde0 homo sapien
O79m48 mus musculu
O71c148 rattus norv
O8tde0 homo sapien
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Result

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331	301	305	304	338	321	322	338	328	343	338	310	310	310
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AAH64040	MGA6_MOUSE	MGA7_MOUSE	Q8N7J6	Q91ZC3	Q7TN38	Q91ZB9	Q8CDY4	Q8IXE2	MRGF HUMAN	Q91ZC2	CAC86257	Q91ZB7	Q711I9
Aah64040 mus muscu	Q91zc6 mus musculu	Q91zc5 mus musculu	Q8n7j6 homo sapien	Srim	Q7tn38 rattus norv		Q8cdy4 mus musculu		Q96am1 homo sapien		Cac86257 mus muscu	Q91zb7 mus musculu	mus

## ALIGNMENTS

RT receptor genes.";  RL Submitted (JUL-2001) to the EMBL/Gent Submitted (JUL-2001) to the EMBL/Gent CC including the sensation or modulity of the sensation or beta-all cc expressing the receptor. Beta-all CC expressing that the receptor could suggesting that the receptor could complay the sense but internalized cc plasma membrane but internalized could cc complay the sense could cc complay the sense could contain the sense contains the	FEBS Lett. 520:97-101(2002).  [4] SEQUENCE FROM N.A. SUNWA M., Sato T., Okouchi I., Arita Suwa M., Sato T., Okouchi H., Asai K., Tsutsumi S., Aburatani H., Asai K., "Genome-wide discovery and analysis	"Identification of a grotein-couresponsive to beta-alanine."; J. Biol. Chem. 279:23559-23564 (200 [3] SEQUENCE FROM N.A. MEDLINE=22040266; PubMed=12044878; Takeda S., Kadowaki S., Haga T., T	SEQUENCE FROM N.A., SUBCELLULAR LOCA SEQUENCE FROM N.A., SUBCELLULAR LOCA TISSUB=Liver; PUSUB=21ver; Pubmed=15037633; DOI=10.1074/jbc.M31 Shinohara T., Harada M., Ogi K., Mai Shinohara T., Komatsu H., Hosoya M., Fukusumi S., Komatsu H., Hosoya M.,	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=22810130; PubMed=12909716; Zylka M.J., Dong X., Southwell A.L. "Atypical expansion in mice of the "Atypical expansion family."; Proc. Natl. Acad. Sci. U.S.A. 100:1		
regulate nociceptor function and/or development, sensation or modulation of pain. Functions as a rane receptor for beta-alanine. Beta-alanine at ses specifically evoked Ca(2+) influx in cells receptor. Beta-alanine decreases forskolin-flap production in cells expressing the receptor, at the receptor couples with G-protein G(q) and G(i). 10 CATION: Integral membrane protein. Localized at the period couples with G-protein G(q) and G(i).	AM., Futami K., Matsumoto S., Akiyama Y.; of human seven transmembrane helix	pled receptor specifically  4).  akaesu H., Mitaku S.; ed receptor genes from the human	OCATION, AND POSSIBLE FUNCTION. M314240200; Maruyama M., Fujii R., Tanaka H., M, Noguchi Y., Watanabe T.,	DOI=10.1073/pnas.1732949100; Anderson D.J.; sensory neuron-specific Mrg G	update) n update) or member D (Beta-alanine )r TGR7). ita; Vertebrata; Euteleostomi;	321 AA.

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EMBL; AB154410; BAD20638.1; -.
EMBL; AB03627; BAB89340.1; -.
EMBL; AB065786; BACC6005.1; AL7
Genew; HGNC:29626; MRGPRD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; F;

PROSITE; PS0262; G PROTEIN RECEP F1 2; 1

G-protein coupled receptor; Glycoprotein;
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Pred. No. 1.4e-117;
Mismatches 0;
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G protein-coupled receptor T
Homo sapiens (Human)
                                                                            sukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
[11]
SEQUENCE FROM N.A.

Shinohara T., Harada M., Ogi K., Maruyama M., Fu Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Moriya T., Itoh Y., Hinuma S.;

"Identification of a G Protein-coupled Receptor Responsive to beta-Alanine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDITINE=22810130; PubMed=12909716;

Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;

"Atypical expansion in mice of the sensory neuron-s
protein-coupled receptor family.";

Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003)

EMBL; AY427820; AAR05120.1; -.
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Metazoa; Chordata; (
Lharia; Primata; C
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Pred. No. 1.4e-117;
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EMBL; AB154410; CRECEPTOR.
SEQUENCE 321 A.
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01-OCT-2004
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J. Biol.
-!- FUNCT
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PubMed=15037633; DOI=10.1074/jbc.M314240200;
Shinohara T., Harada M., Ogi K., Maruyama M., Fy
Pukusumi S., Komatsu H., Hosoya M., Noguchi Y.,
Moriya T., Itch Y., Hinuma S.;
"Identification of G protein-coupled receptor genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Mas-related G-protein coupled receptor member
receptor) (G protein-coupled receptor TGR7).
Name=MRGPRD; Synonyms=MRGD;
Macaca fascicularis (Crab eating macaque) (Cyn
This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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NCBI_TaxID=9541;
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                                                                                                                                                                 Biol. Chem. 279:23559-23564(2004).

FUNCTION: May regulate nociceptor function and/or devel including the sensation or modulation of pain. Function specific membrane receptor for beta-alanine. The recept with G-protein G(q) and G(1) (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Co-expressed in the small diameter with PZX3 and VRI in dorsal root ganglia.

SIMILARITY: Belongs to family 1 of G-protein coupled results.
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BAD20638.1; -.
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Pred. No. 1.4
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1.4e-117;
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                                                                                                                                                              FCIYILNIAAADLLELESMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS
              REEPELEGGETPTVGTNEMGA
                                               WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSI
                                                                                   VQAALIMGVLTEVMTLSSLTLEVMVRRSSQQWREQPTRLEVVVLASVLVELICSLELSIY
                                                                                                             TQRCLSVLFPIWFKCHRPRHLSAWVCALLWMLCLLTNGLTSCFCSKFLKFNKDQCFRVDM
                                                                                                                         TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM
                                                                                                                                                  FSIYILMLAAADLLFVFCMAAMLSLETQPLVSTTDKVHELMKRLKYFAYTVGLSLLTAIS
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REEPELEGGETPTTGTNEMGA
                                    WFVLYWLNLPPDTKVLYFNLSRLSSSMSSSANPLIYFLVGSRRSRRL-QGSLGTVLQRAL
                                                                         VQAALIMGVLTPVMTLSSLTLFVRVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLGFY
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                   86.7%;
88.2%;
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                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).

2 (Potential).

Extracellular (Potential).

3 (Potential).

Cytoplasmic (Potential).

4 (Potential).

Extracellular (Potential).

5 (Potential).

Cytoplasmic (Potential).

6 (Potential).

6 (Potential).

Extracellular (Potential).

7 (Potential).

Extracellular (Potential).
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Pred.
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N-linked (GLCNAc. . .) (Potential).
N-linked (GLCNAc. . .) (Potential).
N-linked (GLCNAc. . .) (Potential).
; 265E137FC7E5481C CRC64;
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                                                                                                                                                                                                                                      1439.5; DB 1
No. 7.6e-101;
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r (Potential).
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RESULT 5
BAD20641 PRELIMINARY; PRT; 320 AA.

ID BAD20641;
AC BAD20641;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE G protein-coupled receptor TGR7.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Mammalia, Butheria; Primates; Craniata; Vertebrata; Euteleostomi;
OC Mammalia, Butheria; Primates; Catarrhini; Cercopithecidae;
OC NOBI TaxID=9541;
RN SEQUENCE FROM N.A.
RA Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.
RA Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.
RA Shinohara T., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,
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RESULT RE
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Best Local S
Matches 283
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Ol-OCT-2004 (Rel. 45, Last sequence update)
Ol-OCT-2004 (Rel. 45, Last sequence update)
Ol-OCT-2004 (Rel. 45, Last annotation update)
Ol-OCT-2004 (Rel. 45, Last annotation update)
Mas related G-protein coupled receptor member D (Be receptor) (G protein-coupled receptor TGR7).
Name=Mrgprd, Synonyms=Mrgd;
Nus musculus (Mouse).
Pukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae
     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.,

Shinohara T., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,

Moriya T., Iroh Y., Hinuma S.,

"Identification of a G protein-coupled receptor specifically
responsive to beta-alanine.",

J. Biol. Chem. 279:23559-23564 (2004).

-1- FUNCTION: May regulate nociceptor function and/or development,

including the sensation or modulation of pain. Functions as a

specific membrane receptor for beta-alanine. The receptor coup

with G-protein G(g) and G(i) (By Similarity).
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Q91ZB8;
                                                                                                                                                                                                                                                                                                                                                                                  nociceptive sensory neurons.";
Cell 106:619-632(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J., "A diverse family of GPCRs expressed in specific subsets of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND TISSUE STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21435808; PubMed=11551509;
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EMBL; AB154413; BAD20641.1;
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"Identification of a G Protein-coupled Receptor Specifically
Responsive to beta-Alanine.";
J. Biol. Chem. 279:23559-23564(2004).
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LOCATION: Integral membrane
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Pred. No. 7.6e
13; Mismatches
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1
G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY042209; AAK91800.1; -.
EMBL; AB154412; BAD20640.1; -.
MGD; MGI:3033142; Mrgprd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement into removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that includes nociceptors. Expressed in the subclass of nonpeptidergic sensory neurons that are IB4(+) and VR1(-).

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                       SLPLSIYWFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLG
                                                                                                   QCFKVDIVFNSLILGIFMPVMILTSTILFIRVRKNSLMQRRRPRRLYVVILTSILVFLTC
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Pred. No. 1.1e
19; Mismatches
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Cytoplasmic ()
6 (Potential)
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N-linked (GlcNAC
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BAD20640

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PRT;

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MRGD_TT 1D
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DT 01-C
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STRAIN-Sprague Dawley;
MEDLINE-22810130; PubMed=12909716; DOI=10.1
Zylka M.J., Dong X., Southwell A.L., Anders
"Atypical expansion in mice of the sensory
protein-coupled receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 100:10043-100
[2]
                                                                                                                                                                                                                                                                                   ORGD RAT STANDARD; PRT; 319 AA. Q7TN41; Q6L788; O1-OCT-2004 (Rel. 45, Created) O1-OCT-2004 (Rel. 45, Last sequence update) O1-OCT-2004 (Rel. 45, Last annotation update) O1-OCT-2004 (Rel. 45, Last annotation update) Mas-related G-protein coupled receptor member D receptor) (G protein-coupled receptor TGR7). Name=Mrgprd; Synonyms=Mrgd;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukusumi S., Komatsu H., Hosoya M., Nog
Moriya T., Itoh Y., Hinuma S.;
"Identification of a G Protein-coupled
Responsive to beta-Alanine.";
J. Biol. Chem. 279:23559-23564 (2004).
EMBL; AB154412; BAD20640.1; -.
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01-JUN-2004
01-JUN-2004
                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            Rattus norvegicus
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Shinohara T., Harada
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Ol-JUN-2004 (TrEMBLrel. 27, Last sequence update)
Ol-JUN-2004 (TrEMBLrel. 27, Last annotation updat
G protein_coupled receptor TGR7.
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Rodentia;
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9; Mismatches
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Pred. No. 1.1
                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
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Sciurognathi;
                        100:10043-10048(2003)
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M., Noguchi Y., Watanabe
                                                               DOI=10.1073/pnas.1732949100;
., Anderson D.J.;
sensory neuron-specific Mrg
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les 73;
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e T.,
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MNQTLNSSG----TVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGF-R

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MNYTPYSSPAPGLTISPTMD-----PVTWVYFSVTFLAMATCVCGIVGNSMVIWLLSFHR

56 MHRNDFCIYILNLAAADLLFLFSMASTLSLETQPLV--NTTDKVHELMKRLMYFAYTVGL

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Query Match
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                                                 SEQUENCE
                                                                                                                                                                                                                                            G-protein
DOMAIN
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                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                          InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a G protein-coupled receptor specifically responsive to beta-allanine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukusumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinohara
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                                                                                                                                                          TRANSMEM
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Biol. Chem. 279:23559-23564 (2004).

FUNCTION: May regulate nociceptor function and/or development, including the sensation or modulation of pain. Functions as a specific membrane receptor for beta-alanine. The receptor coup: with G-protein G(q) and G(i) (By similarity).

**SUBCELLULAR LOCATION: Integral membrane protein.

**TISSUB SPECIFICITY: Co-expressed in the small diameter neurons with P2X3 and VRI in dorsal root ganglia.

**SIMILARITY: Belongs to family 1 of G-protein coupled receptors was expressed.
                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restroy by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                               738040; Mrgprd.
 191;
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            Similarity
                                                                                                                                                                                                                                         PS00237; G_PROTEIN RECEP_F1_1; FALSE_NEG.
PS50262; G_PROTEIN RECEP_F1_2; 1.
n_coupled_receptor; Transmembrane.
1 30 Extracellular (Potent
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                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633; DOI=10.1074/jbc.M314240200; Harada M., Ogi K., Maruyama M., F. Komatsu H., Hosoya M., Noguchi Y., toh Y., Hinuma S.;
                                                Å
                                                                                                                                                         35830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND TISSUE SPECIFICITY.
          55.2%;
                                                 ¥.
 48;
Score 917.5;
Pred. No. 2.1e
48; Mismatches
                                                                                 Cytoplasmic (Pocential).

Cytoplasmic (Pocential)

Extracellular (Potential)

Cytoplasmic (Pocential)

Cytoplasmic (Potential)

Extracellular (Potential)

Cytoplasmic (Pocential)

Cytoplasmic (Pocential)

Cytoplasmic (Pocential)

Cytoplasmic (Pocential)
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Matches 190
              MRG4 HUMAN STANDARD; PRT; 322 AA. 096LA9; Q8TDD6; 01-OCT-2004 (Rel. 45, Created) 01-OCT-2004 (Rel. 45, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Mas-related G-protein coupled receptor member specific G-protein coupled receptor 6).

Name=MRGX4; Synonyms=SNSR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinohara T., Harada M., Ogi K., Maruya Fukusumi S., Komatsu H., Hosoya M., Nog Moriya T., Itoh Y., Hinuma S.; "Identification of a G Protein-coupled Responsive to beta-Alanine."; Biol. Chem. 279:23559-23564 (2004). EMBL; AB154411; BAD20639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-JUN-2004
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                                                                                                                                                                                                                                                                                                                              SLPLSIYWFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLG
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27, Last sequence update)
27, Last annotation update)
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Pred. No. 5.
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Noguchi Y.,
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CONFLICT

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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI_TaxID=9606;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=2195373; PubMed=11850634; DOI=10.1038/nn815;
Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D.,
Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M.,
Zhang J., Fortin Y., Banville D., Shen S., Stroem P.,
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MEDLINE=21435808; PubMed=11551509;

Dong X., Han S.-K., Zylka M.J., Simon
"A diverse family of GPCKs expressed i
"nociceptive sensory neurons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY042216; AAK91807.1;
EMBL; AF474992; AAL86883.1;
MIM; 607230; -.
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                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
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PRINTS: PROUZ37; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEPTOR; Polymorphism; G-protein coupled receptor; Glycoprotein; Polymorphism; G-protein coupled receptor; Glycoprotein coupl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Proenkephalin A gene products activate a new family of sensory neuron-specific GPCRs.";
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                                                                                                                        VARIANT
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                                                                 VARIANT
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                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                            DOMAIN
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TISSUE SPECIFICITY: Uniquely localized in a subset of small dor root and trigeminal sensory neurons.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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FUNCTION: Orphan receptor. Probably involved nociceptive neurons. May regulate nociceptive
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                                                                 F -> L (in dbSNP:2468774).

/FTId=VAR 019435.

N -> K (in dbSNP:2445180).

/FTId=VAR 019436.

Y -> C (in dbSNP:1869788).
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Extracellular
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Cytoplasmic (Potential N-linked (GlcNAc...) N-linked (GlcNAc...)
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in specific subsets
                    dbSNP:2445179)
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Labarre M.,
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Best Local S
Matches 135
                                                                                                                                                                                                                                 "Proenkephalin A gene product's activate a new family of senso neuron-specific GPCRs.";

Nat. Neurosci. 5:201-209(2002).

-!- FUNCTION: Orphan receptor. Probably involved in the funct nociceptive neurons. May regulate nociceptor function and development, including the sensation or modulation of pai potently activated by enkephalins (By similarity).

-!- SUBCELULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: Uniquely localized in a subset of smaroot and trigeminal sensory neurons.

-: SINILARITY: Belongs to family 1 of G-protein coupled rece
       entities
or send a
               This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-UCT-2004 (Rel. 45, Last sequence update)
Sensory neuron-specific G-protein
Name=SNSR5;
Homo ---
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SNS5_HU
Q8TDD7;
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MEDILINE=21853733, PubMed=11850634; DOI=10.1038/nn815;
Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., I
Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., I
Gosselin M., Fortin Y., Banville D., Shen S., Stroem P.,
Dray A., Walker P., Ahmad S.;
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Mammalia; Eutheria;
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56; Mismatches
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, Payza i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sensory
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Labarre M.,
                                                                                                                                                                                                                                    receptors.
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noutstation -
                                            .ch/announce/
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RESULT 12
SNS3-IDMAN
ID SNS3
AC QBTDI
O1-OC
DT 01-OC
DT 01-OC
DT SEEBS
GN Names
OS Homo
OC Eukaa
OC Mamma
OX NCBI
RN (1)
RP SEQUE
RX Lembo
RA Lembo
RA GOSSE
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Best Local Similarity
Matches 138; Conserv
                                                                                                                                          SNS3 HUMAN
Q8TDD9;
01-OCT-2004
01-OCT-2004
01-OCT-2004
                                                                                                                 U1-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Sensory neuron-specific G-protein coupled ro
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

MEDILINE=21853733, PubMed=11850634; DOI=10.1038/nn815;
Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., 1
Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., 1
Gosselin M., Fortin Y., Banville D., Shen S., Stroem P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
TRANSMEM
                                                                     NCBI_TaxID=9606;
                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                         HUMAN
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DOMAIN
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DOMAIN
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TRANSMEM
DOMAIN
TRANSMEM
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PROSITE; PS00237; G. PROTEIN RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane.

DOMAIN

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1

PXTracellular
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InterPro; IPR000276; GPCR_R
                                                                                                                                                                                                                                                       283
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                                                                                                                                                                                                                                                       NRONLKLVLORALODKPEVDKGE
                                                                                                                                                                                                                                                                                                                  CSLPLSIYWFVLYWLSLPPB-----MQVLCFSLSRLSSSVSSANPVIYFLVGSRRSHRL
                                                                                                                                                                                                                                                                                                                                                 WCETSDFIPVAWLI-FLCVVLCVSSLVLLVRILCGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNOTINSSGTVESALNYSRGSTVHTAYLVLSSLAMFTC---LCGMAGNSMVIWLLGFRMH
                                                                                                                                                                                                                                                                           PTRSLGTVLQQALREEPELEGGE
                                                                                                                                                                                                                                                                                                    CGLPFGILGALIYRMHLNLEVLYCHVYLVCMSL---
                                                                                                                                                                                                                                                                                                                                                                                               LSAISTERCLSVLWPIWYRCRRPTHLSAVVCVLLWGLSLLFSMLEWRFCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDPTVPVLGTKLTPIN---
                                                                                                                                                                                                                                                                                                                                                                      -CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLVFLI
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322
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42.7%;
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5 (Potential).
Cytoplasmic (Potential).
6 (Potential)
Extracellular (Potential).
7 (Potential).
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2 (Potential)
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
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Pred. No. 3.4e-33;
3; Mismatches 101;
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N-linked (G
                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                   Hominidae;
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                                                                                              Euteleostomi;
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           Roy M.-O.,
Labarre M.,
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Best Local S
Matches 136
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"proenkephalin A gene p
neuron-specific GPCRs."
Nat. Neurosci. 5:201-20
-!- FUNCTION: Orphan re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF474989; AAL86880.2; -.
InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                      SEQUENCE
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SIMILARITY: Belongs to family 1 of G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurosci. 5:201-209(2002).
FUNCTION: Orphan receptor. Probably involved in the functions or negutive neurons. May regulate nociceptor function development, including the sensation or modulation of development, including the sensation or modulation of development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute. The by non-profit institutions as long
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(3)
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PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00237; G_PROTEIN_RECEP_F1_1; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
n coupled receptor; Glycoprotein;
FLICSLPLSIYWFVLYWLSLPPEMQVLC--FSLSRLSSSVSSSANPVIYFLVGSRRSHRL
                                                                                                                 LSILTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNE
                                                                                                                                                            RNPECIYILNLAAADLLFL-----FSMASTLSLETQPLVNTTDKVHBLMKRLMYFAYTVG
                                                                                                                                                                                                                        MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTC---LCGMAGNSMVIWLLGFRMH
                                       DSAWCQTSDFITVAWLI-FLCVVLCGSSLVLLIRILCGS---RKIPLTRLYVTILLTVLV
                                                            DR--CERVDMVQAALIMGVLTEVMTLSSLTLEVWVRRSSQQWRRQP-TRLEVVVLASVLV
                                                                                         LSFLSAVSTERCLSVLWPIWYRCHRPTHLSAVVCVLLWALSLLRSILEWMLCG-FLFSGA
                                                                                                                                             RNAFSIYILNLAAADFLFLSGRLIYSLLSFISI-----PHTISKILYPVMMFSYFAG
                                                                                                                                                                                                MDPTVS---TIDTELTPINGTEETLCYKQTLSLTVLTCIVSLVGLTGNAVVLWLLGCRMR
                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                      Ahmad
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Extracellular (Potential).
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Pred. No. 9
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3 (Potential).
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7 (Potential).
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RESULT
MRG1_H
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 MRG1 HUMAN STANDARE
Q96LB2; Q8TDB;
01-OCT-2004 (Rel. 45, C
01-OCT-2004 (Rel. 45, I
01-OCT-2004 (Rel. 45, I
01-OCT-2004 (Rel. 45, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 13
_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nn815;

Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., I

Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., I

Gosselin M., Fortin Y., Banville D., Shen S., Stroem P.,

Dray A., Walker P., Ahmad S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2004 (Rel. 45, Last annotation update)
Mas-related G-protein coupled receptor member
specific G-protein coupled receptor 4).
Name=MRGX1; Synonyms=SNSR4;
                                                                                                                                                                                                                                                                                                                          receptor genes.".
Submitted (JUL-20
-!- FUNCTION: Or
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Suwa M., Sato T., Okouchi I
Tsutsumi S., Aburatani H.,
"Genome-wide discovery and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome sequence.";
FEBS Lett, 520:97-101(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nociceptive sensory neurons.";
Cell 106:619-632(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takeda S., Kadowaki S., Haga T., Take
"Identification of G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Proenkephalin A gene products activate a new neuron-specific GPCRs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21435808; PubMed=11551509;
Dong X., Han S.-K., Zylka M.J., Simon
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                                                                                                                                        FUNCTION: Orphan receptor. Probably involved in the function of nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain. Potently activated by enkephalins including BAM22 (bowine adrenal medulla peptide 22) and BAM (8-22). BAM22 is the most potent compound and evoked a large and dose-dependent release of intracellular calcium in stably transfected cells. G(alpha) q proteins are involved in the calcium-signaling pathway. SUBCELULUAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeninal sensory neurons.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                               Mas subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X., Han S.-K., Zylka M.J., Simon
iverse family of GPCRs expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288
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ki S., Haga T., Takaesu H., Mitaku
                                                                                                                                                                                                                                                                                                                                                                            Okouchi I., Arita M., Futa
atani H., Asai K., Akiyama
overy and analysis of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Ffam; pF00001; 7cm 1; 1.

PRINTS; pR00237; GFCRRHODDPSN.

PROSITE; pS00237; G_PROTEIN RECEP_F1_2; 1.

PROSITE; pS00237; G_PROTEIN RECEP_F1_2; 1.

PROSITE; pS00262; G_PROTEIN TECEP_F1_2; 1.

STORE TO THE PROPERTY OF T
                                                                          Q7TN42 PRELIMINARY; PRT;
Q7TN42;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last seg
01-MAR-2004 (TrEMBLrel. 26, Last ann
MRGC G protein-coupled receptor.
       Rattus norvegicus ()
Eukaryota; Metazoa;
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SEQUENCE
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EMBL; AF474990; AAL86881.1;
EMBL; AB083628; BAB89341.1;
EMBL; AB065846; BAC06064.1;
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Pred. No. 9.6e-33;
9; Mismatches 100;
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N-linked (GlcNAc. .) (Po
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C7F3A9F4418E8AD1 CRC64;
                                                                                                   sequence update)
annotation update
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       Vertebrata;
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       Euteleostomi;
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SEQUENCE
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MEDLINE=22810130; Puby
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31; Conservative
                                                                                                      SUTVMVYLICGLPLGLYLFLLYWFGIHLHYPFCHI--YQVTVLLSCVNSSANPIIYFLVG
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SFR-HRKKHRSLKMVLKRALEETPE
                                                 SRRSHRLPTRSLGTVLQQALREEPE
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Pred. No. 1e-31;
7; Mismatches
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Q96LB1;
01-OCT-2004
01-OCT-2004
01-OCT-2004
                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                             Mas-related G-protein Name=MRGX2;
                                                                                                                                                                                                                                        HUMAN
MRG2_I
                                 MEDLINE=21435808; PubMed=11551509;
Dong X., Han S.-K., Zylka M.J., Simon
"A diverse family of GPCRs expressed :
nociceptive sensory neurons.";
SEQUENCE
                                                                                                                                                  Homo
                                                                                    EQUENCE FROM N.A.
                        106:619-632(2001).
                                                                                                                                                 sapiens (Human).
                                                                                                                                                                                                                                        HUMAN
FROM N.A
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                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update
                                                                                                                                                                         coupled
                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                        receptor
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RA Klausherg R.D., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Klausher R.D., Collins F.S., Debeng L., Shemmen C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abzamson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,
RGeneration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ",
Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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PubMed=12915402; DOI=10.1074/jbc.M302456200;
Robas N., Mead E., Fidock M.;
"MrgX2 is a high potency cortistatin recepto
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                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler
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Tsutsumi S., Aburatani H.,
"Genome-wide discovery and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Suwa M., Sato T.,
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Takeda S., Kadowaki S., Haga T., Takaesu
           EMBL;
EMBL;
MIM; 6
                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Orphan receptor. Probably involved in the function of nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain. Cortistatin-14 seems to be a high potency ligand at this receptor. Cortistatin has several biological functions including roles in sleep regulation locomotor activity, and cortical function. In receptor-expressing cells, cortistatin-stimulated increases in intracellular Ca(2+) but had no effect on basal or forskolin-stimulated CAMP levels, suggesting that this receptor is G(q)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coupled.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Has a limited expression profile, both
peripheral and within the central nervous system, with highest
levels in dorsal root ganglion.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mas subfamily.
AY042214;
; AB083626;
; AB065811;
; BC063450;
607228; -.
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                                                             AAK91805.1;
BAB89339.1;
BAC06030.1;
AAH63450.1;
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atani H., Asai K.,
overy and analysis
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Akiyama Y.;
of human seven transmembrane helix
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Best Local Sim
Matches 133;
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PRINTS; PR00237; GPCRREIDODESN.
PROSITE; PS00237; G PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
PROSITE: PS50262; G PROTEIN_RECEP_F1_2; 1.
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                                                                                                                          GLSNLSTVSTERCLSVLWPIWYRCRRPRHLSAVVCVLLWALSLLLSILEGKFCG-FLFSD
                                                                                                                                              GTSTTATSTORCTSATESIMEKCHEBEHTSAMACGTTMLTCTTWNGTLSSECSKETKEN
                                                                                                                                                                   GFRMRRNAFSVYVLSLAGADFLFLCFQIINCLVYLSNFFCSISINFPSFFTTVMTCAYLA
                                                                                                                                                                                      GERMHRNPFCIYILNLAAADLLEL-ESMASTLSLETQPLVNTTDKVHELMKRLMYFAYTV 111
                                                                                                                                                                                                           MDPTTPAWGTESTTVNGN-----DQALLLLCGKETLIPVFLILFIALVGLVGNGFVLWLL
                                                           VFLICSLPLSIYWFVLYWLSLPPEMQVLC--FSLSRLSSSVSSSANPVIYFLVGS-RRSH
                                                                                 GDSGWCQTFDFITAAWLI-FLFMVLCGSSLALLVRILCGS---RGLPLTRLYLTILLTVL
RLQQPILKLALQRALQDIAEVDHSEGCFRQGTPEMSRSSL
                     RLPTRSLGTVLQQALREEPELEGGE----TPTVGTNEM
                                        VFLLCGLPFGIQWFLILWIWKDSDV-LFCHIHPVSVVLSSLNSSANPIIYFFVGSFRXQW
                                                                                                     EDR--CFRVDMVQAALIMGVLTPVMTLSSLTLFVMVRRSSQQWRRQP-TRLFVVVLASVL
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39.1%;
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Cytoplasmic (Potential).
Extracellular (
7 (Potential).
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2 (Potential).
Extracellular
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Pred. No. 1.7e-31
                                                                                                                                                                                                                                                                                                                    Cytoplasmic
N -> S (in c
                                                                                                                                                                                                                                                                                                                                                                                             Extracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
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1=VAR_019433.
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                                                                                                                                                                                                                                                                            Length 330
                        319
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Search completed: November Job time: 194 secs 2004, 11:05:53

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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1661
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. / yurz b/ptodata/1/pubpaa/US09A PUBCOMB.pep:*
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1: /cgn2_6/ptodata/1/pubpaa/US09C PUBCOMB.pep:*
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1: /cgn2_6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*
1: /cgn2_6/ptodata/1/pubpaa/US10C PUBCOMB.pep:*
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1: /cgn2_6/ptodata/1/pubpaa/US60 PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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cgn2_6/ptodata/1/pubpaa/US09A
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Sequence 8, Appli			Sequence 4, Appli		Sequence 1, Appli	Sequence 1050, Ap	Sequence 8, Appli		Sequence 2, Appli	Sequence 268, App	Sequence 2, Appli	Description		

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1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

0.0 321 15 US-10-314-040A-1 0.0 321 16 US-10-314-040A-1 0.0 321 16 US-10-312-807-10 0.0 321 16 US-10-312-807-10 0.0 321 16 US-10-26-248-34 4.6 307 9 US-09-816-087-2 4.6 307 14 US-10-305-555-3 6.7 307 14 US-10-305-555-3 6.8 321 15 US-10-305-555-3 6.8 321 14 US-10-305-555-3 6.8 321 14 US-10-305-555-3 6.8 321 14 US-10-292-798-10 6.8 322 14 US-10-292-798-10 6.9 322 14 US-10-292-798-10 6.0 322 14 US-10-292-798-8 6.0 322 15 US-10-072-012-52
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5 US-10-343-807-10 6 US-10-314-048A-10 6 US-10-314-048A-10 6 US-10-314-048A-10 6 US-10-016-248-3-2 US-09-816-087-2 4 US-10-305-555-3 5 US-10-116-248-80 US-10-305-555-3 6 US-10-10-292-798-004 US-10-292-798-004 US-10-292-798-004 US-10-292-798-004 US-10-292-18 10-10-292-798-004 10-10-292-798-004 10-10-292-798-4 10-10-10-116-116-105 10-10-292-798-898 10-10-072-012-536 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535 10-10-072-012-535
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## ALIGNMENTS

US-09-920-068A-2

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Sequence 2, Application US/09920068A
; Patent No. US20020116724A1
; GENERAL INFORMATION:
APPLICANT: Wolf, Eckhard
APPLICANT: Wolf, Eckhard
APPLICANT: Welf, Eckhard
APPLICANT: Welf, Eckhard
APPLICANT: Welf, Eckhard
APPLICANT: Welfer, Sabine
APPLICANT: Regenbogen, Johannes
APPLICANTON INVENTION: Pharmacologically Active Substances
FILE OF INVENTION: Use for the Diagnosis or Treatment of Disorders, for example
TITLE OF INVENTION: Skin Disorders and their Use for the Identification of
FILIZ OF INVENTION: Pharmacologically Active Substances
FILE REFERENCE: 50125/015002
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US/09/920,068A
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US/09/920,068A
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US/09/920,068A
CURRENT FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 21
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 21
SOFTMARE: FastSEQ for Windows Version 4.0
Length 321;
US-09-920-068A-2
Query Match
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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180

300

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Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 268
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
US-09-801-944B-268
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US-09-801-944B-268
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PRIOR FILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/187,715
PRIOR PPLICATION NUMBER: 60/187,715
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/187,825
PRIOR PPLICATION NUMBER: 60/187,825
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/187,833
PRIOR APPLICATION NUMBER: 60/187,833
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
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Best Local S
Matches 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Vogeli, Gabriel
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: No. US20040014169A1el G Protein-Coupled Receptors
FILE REFERENCE: 00100US1
CURRENT APPLICATION NUMBER: US/09/801,944B
CURRENT FILING DATE: 2003-08-01
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/187,582
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/187,581
PRIOR FILING DATE: 2000-03-08
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                       61
                                                                                                                                    2h 100.0%; Score 1661; DB 11; Similarity 100.0%; Pred. No. 1.3e-145; 21; Conservative 0; Mismatches 0;
FCIYILNLAAADLLFLFSWASTLSLETQPLVNTTDXVHELMKRLMYFAYTVGLSLLTAIS
                                                                                    MNQTINSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP
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                                                                                                                                                                              Length 321;
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Publication No. US20030082585A1

GENERAL INFORMATION:
APPLICANT: Tian, Hui
APPLICANT: Dai, Kang
APPLICANT: Chen, Jin-Long
APPLICANT: Chen, Jin-Long
APPLICANT: Tularik Inc.
TITLE OF INVESTION: No. US20030082585A1el Receptors
FILE REFERENCE: 018781-008410US
CURRENT APPLICATION NUMBER: US/10/188,405
CURRENT APPLICATION NUMBER: US/07-01
PRIOR APPLICATION NUMBER: US/07-03
JUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
TYPE: PRI
CREMITM: Unc. capitan.
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                                            REEPELEGGETPTVGTNEMGA 321
                                                                                    WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL
                                                                                                             WFVLYWLS1PPEMQVLCFS1SRLSSSVSSSANPVIYFLVGSRRSHRLPTRS1GTVLQQAL
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APPLICANT: SYNA, MALK
APPLICANT: HAN, SANG-KYOU
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTEL 4C1CP1
CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-05-04
NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
NUMBER: OF SEQ ID NOS: 109
SCETWARE: FASTSEQ for Windows Version 4.0
LENGTH: 321
TYPE: DET
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US-10-079-384-8
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Sequence 8, Application US/10079384
Publication No. US20030108986A1
GENERAL INFORMATION:
APPLICANT: Communi, Didier
TITLE OF INVESTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 9409/2132
CUCRENT APPLICATION NUMBER: US/10/079,384
CURRENT FILING DATE: 2002-02-20
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Publication No. US20030092035A1
GENERAL INFORMATION:
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APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark
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Simon, Melvin
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100.0%; Pred. No. 1.3e-145;
7ative 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-079-384-8
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US-10-017-161-1050
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Best Local :
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Best Local Similarity 100.0%;
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  FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS
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PRIOR APPLICATION NUMBER: US 09/885,453
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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                                                    WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
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WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSI
                                                                                                              VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY
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Pred. No. 1.3e-145;
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APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ABUDATANI, HIROYUKI
ITILE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/10/046789
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1050
LENGTH: 321
TYPE: PRT
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                                                                                                                     h 100.0%; Score 1661; DB 14; Similarity 100.0%; Pred. No. 1.3e-145; 21; Conservative 0; Mismatches 0;
MOTINSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP
                                                         MNOTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP
                                                                                                                         Indels
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APPLICANT: SHINTANI, Yashushi
APPLICANT: SHINTANI, Yashushi
APPLICANT: MATSUI, Hideki
TITLE OF INVENTION: NO. US20030153040A1el G Profile Reference: 2721 US0P
CURRENT APPLICATION NUMBER: US/10/258,768
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: PCT/JP01/03597
PRIOR APPLICATION NUMBER: D7 2000-130478
PRIOR FILING DATE: 2001-4-26
PRIOR FILING DATE: 2000-4-28
PRIOR APPLICATION NUMBER: JF 2000-130478
PRIOR APPLICATION NUMBER: JF 2000-140435
PRIOR APPLICATION UMBER: JF 2000-140435
PRIOR APPLICATION UMBER: JF 2000-140435
PRIOR FILING DATE: 2000-5-12
NUMBER OF SEQ ID NOS: 7
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US-10-258-768-1
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; ORGANISM: Human
US-10-258-768-1
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publication No. US20030153040A1
GENERAL INFORMATION:
APPLICANT: MORIIVA, Takeo
APPLICANT: ITO, Takashi
APPLICANT: SHINTANI, Yashushi
APPLICANT: NATANI, Yashushi
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SEQ ID NO 1
LENGTH: 321
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Best Local
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Sequence 2, Application US/10239421

Sequence 2, Application US/10239421

Publication No. US2030153498A1

GENERAL INFORMATION:
APPLICANT: Shyman Ramakrishnan
TITLE OF INVENTION: REGULATION OF HUMAN RTA-LIKE G F
FILE REFERENCE: 004974.00798

FILE REFERENCE: 004974.00798

CURRENT APPLICATION NUMBER: US/10/239,421

CURRENT FILING DATE: 2002-09-23

PRIOR APPLICATION NUMBER: 60/191,765

PRIOR APPLICATION NUMBER: 60/191,765

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 321
; SEQ ID NO 4
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo s
US-10-305-555-4
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US-10-305-555-4
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US-10-239-421-2
                                                                                                 Sequence 4, Application US/10305555

Publication No. US20030157525A1

Publication No. US20030157525A1

GENERAL INFORMATION:

APPLICANT: Bristch-Myers Squibb Company

ITILE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY31, AND VARIANTS;

TITLE OF INVENTION: NETHODS OF USE THEREOF

FILLE REFERENCE: D0196 NP

CURRENT APPLICATION NUMBER: US/10/305,555

CRURARI FILING DATE: 2002-11-26

PRIOR APPLICATION NUMBER: U.S. 60/333,337

PRIOR APPLICATION NUMBER: U.S. 60/355,619

PRIOR APPLICATION NUMBER: U.S. 60/355,619

PRIOR FILING DATE: 2002-02-06

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.1
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Query Match

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; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo s
US-10-088-726-19
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: PCT/JP00/09408
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 1999-375152
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-8
PRIOR APPLICATION NUMBER: JP 2000-101339
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 63
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US-10-088-726-19
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SEQ ID NO 19
LENGTH: 321
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Publication No. US20030157558A1
GENERAL INFORMATION:
APPLICANT: Matsumoto et al.
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS
TITLE OF INVENTION: THEREOF, AND PRODUCTION AND USES THEREOF
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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/9/714,008
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1999-11-17
PRIOR PELLING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,099
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,369
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,369
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/171,902
PRIOR APPLICATION NUMBER: 60/171,901
PRIOR APPLICATION NUMBER: 60/171,901
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/181,749
PRIOR APPLICATION NUMBER: 60/181,749
PRIOR APPLICATION NUMBER: 60/181,749
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/181,749
PRIOR FILING DATE: 2000-02-11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-10
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US-10-321-807-10
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chen, Rupong
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Receptors
FILE REFERENCE: ARENO866
FILE REFERENCE: ARENO866
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WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL
                                                 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY
                                                                                                                                  TORCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM
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No. US20030166148A1
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US-10-237-467-8
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                Sequence 18, Application US/10182822A
Publication No. US20030211493A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.
APPLICANT: AU-YOUNG, JANICE; YUE, HENTY
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0032 USN
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LENGTH: 321
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Best Local
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FILE REFERENCE: 021288-001300US
CURRENT APPLICATION NUMBER: US/10/237,467
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/317,879
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Gray, Nathanael S.
APPLICANT: Caldwell, Jeremy C.
APPLICANT: Schultz, Peter G.
APPLICANT: IRM LLC
CURRENT
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APPLICATION NUMBER: US/10/182,822
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Conservative 0;
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Pred. No. 1.3e-145;
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CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: PCT/US 01/03455
PRIOR PTLING DATE: 2001-01-02
PRIOR PLIING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: US 60/182,045
PRIOR PLIING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 321
                                                                                                 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-343-650A-42
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US-10-343-650A-42
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Best Local Similarity 100.0%; Score 1661; DB 15; Matches 321; Conservative 0; Mismatches
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application US/10343650A Fublication No. US20040067499A1 GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-185347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7472136CD1
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ORGANISM: Homo sapiens
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                                                              DB 15;
                                                            Length 321;
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MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP

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CURRENT APPLICATION NUMBER: US/10/321,807
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/99/714,008
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1999-11-17
PRIOR PILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,099
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,369
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/171,902
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/171,901
PRIOR APPLICATION NUMBER: 60/181,749
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US-10-321-807-10
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                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
S-10-321-807-10
                                                                                      Query Match 100.0%; Score 1661; DB 16; Length 321; Best Local Similarity 100.0%; Pred. No. 1.3e-145; Matches 321; Conservative 0; Mismatches 0; Indels 0;
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Publication No. US20040137563A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chen, Rupong
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN0086
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MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
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Search completed: November 4, 2004, 11:17:21 Job time: 148 secs

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## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
בו	1661	00	321	4	929	Aau19292 Human G p
N	99	0	321	4.	AAG65582	g65582 Human
ω	1661	00.	321	4	576	e06768 Human
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Adc17728	Aay87664	Aay30164	Ado29706	Adh08537	Adc17723	Abp81758	Abp96692	Adi16995	Adi17000	Aae21297	Abj04076	Aay87663			Aae21305	Add29436	Aay90513	Ado29547	Aay77734
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## ALIGNMENTS

Human; G protein-coupled receptor; nGPCR-x; antiviral; analgesic; cytostatic; cardiant; antidiabetic; anoretic; hypotensive; hypertensive; antiparkinsonian; nootropic; neuroprotective; antidepressant; viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain; cancer; metabolic disease; cardiovascular disease; type 2 diabetes; obesity; anorexia; hypotension; hypertension; myocardial infarction; atherosoles parkinson's disease; psychosis; neurological disorder; schizophrenia; migraine; major depression; anxiety; mental disorder; schizophrenia; migraine; major depression; anxiety; mental disorder; manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome. AAU19292 standard; protein; 321 Homo sapiens. Human G protein-coupled receptor nGPCR-74. 04-DEC-2001 AAU19292; (first entry) Ä

WO200166750-A2.

13-SEP-2001.

08-MAR-2001; 2001WO-US007322.

08-MAR-2000 08-MAR-2000; 08-MAR-2000; 08-MAR-2000; 2000US-0187581P.
2000US-0187582P.
2000US-0187715P.
2000US-0187825P.
2000US-0187825P.
2000US-0187829P.
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2000US-0187830P.
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2000US-0187830P.
2000US-0187939P.
2000US-0187928P.
2000US-0187939P.
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2000US-0187939P.

(PHAA) PHARMACIA & UPJOHN CO

2000US-0189294P.

Vogeli G, Wood LS;

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Best Local S
Matches 321
           rungicide; protozoacide; cytostatic; antibacterial; virucide; hypotensive; antiallergic; antiulcer; analgesic; osteopathic; cardian; neuroprotective; nootropic; anticonvulsant; neurolentic.
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N-PSDB; AAS30861.
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                                                                                                                          Human RTA-like G protein-coupled receptor polypeptide
                                                                                                                                                                                                                                          AAG65582 standard;
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Pred. No. 7.3e-181;
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cc polypeptide. The RTA-like GPCR polypeptide can be expressed by standard compositions comprising the composition of the methodology. Pharmaceutical compositions comprising the polypeptide or its modulators are useful for modulating the activity of composition pain, cancer, and as bacterial, fungal, protozoan and viral infection, pain, cancer, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypotension, urinary retention, completely consist, angina pectoris, myocardial infarction, ulcer, allergy, comultiple sclerosis, benign prostatic hypertrophy, and psychotic and neurological disorder, mental retardation and dyskinesia such as compound which may act as continuous for an allergy are intributed in an adjoint at the receptor sites, for raising specific contributed which can block the receptor, and as bait protein in a two-chybrid or three-hybrid assay. Modulators of the polypeptide are useful in treating various physiological disorders relating to abnormal control of abnormal angiotensin-induced aldosterone secretion, and in reversing cardiovascular ailments such as caused by excessive pulmonary blood flow correction.
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Matches 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypotension
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REEPELEGGETPTVGTNEMGA
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Mismatches 0;
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Human; G-protein coupled receptor-18; GCREC-18; cytostatic; hepatotropic; virucide; antiinflammatory; anticonvulsant; antiemetic; neuroprotective; nootropic; cerebroprotective; hypotensive; tranquilliser; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; antorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease; huntington's disease; Parkinson's disease; cardiovascular disorder; epilepsy; hypertension; varicose vein; vasculitis; dysphagia; dyspepsia; anorexia; gastrointestinal disorder; panoreatitis; autoimmune disorder; Addison's disease; Crohn's disease; acquired immune deficiency syndrome; AIDS; uveitis; infection; trauma; metabolic disorder; diabetes; obesity;
                                                    The present sequence is human G-protein coupled receptor-18 (GCREC-18) protein. The present invention relates to GCREC protein and nucleic acids encoding them. GCREC protein, its agonist or antegonist are useful for treating diseases or conditions associated with decreased expression or overexpression of functional GCREC in a patient, where the disorder is selected from cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis cirrhosis, hepatitis, psoriasis, and cancer, neurological disorders such as epilepsy, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease, Cardiovascular disorders such as hypertension, vasculitis, variose veins, gastro-
intestinal disorders such as dysphagia, dyspepsia, anorexia, nausea, pancreatitis, autoimmune/inflammatory disorders such as acquired immunodeficiency syndrome (AIDS), Addison's disease, Crohn's disease,
                                                                                                                                                                                                                                                                                               Novel isolated human G-protein coupled receptor useful for diagnosing, preventing and treating cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory and metabolic disorders.
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11-FEB-2000; 2000US-0182045P.
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RESULT 4
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AAG64126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; guanosine triphosphate binding protein-coupled receptor; grotein-coupled receptor; GPRv12; GPRv13; GPRv14; GPRv51; GPRv71; GPRv72; cancer; liver cirrhosis; Alzheimer's disease; cytostatic; hepatotropic; nootropic;
                           Matsumoto S,
Sugiyama T,
                                                                                                                                                       28-DEC-1999;
31-MAR-2000;
                                                                                                                                                                                                                                 28-DEC-2000; 2000WO-JP009408
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Kishimoto
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zaki K, Yasuda
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la S, Ino
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RESULT 5
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Best Local S
Matches 321
  17-NOV-1999;
17-NOV-1999;
17-NOV-1999;
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                                                                                                                                                                 25-MAY-2001
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                                                                                                          16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                inverse
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se agonist;
                                                                                                                                                                                                                                                                                                                                                                                                           G-protein
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                                                                                                             2000WO-US031509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
99US-0166088P.
99US-0166099P.
99US-0166369P.
                                                                                                                                                                                                                                                                                                                                                                                                              coupled receptor,
                                                                                                                                                                                                                                                                                                                        coupled receptor; GPCR; hRUP12;
lung cancer.
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Pred. No. 7.3e-181;
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23-DEC-1999;
23-DEC-1999;
11-FEB-2000;
14-MAR-2000;
14-MAR-2000;
10-APR-2000;
10-APR-2000;
10-APR-2000;
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12-JUN-2000;
21-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a human G-protein coupled receptor (GPCR), hRUP12. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists inverse agonists or partial agonists for use as therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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20-OCT-2000;
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12-MAY-2000;
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                                WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL
                                                                                          VQAALIMGVLTPVWTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY
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99US-0171901P.
99US-0171902P.
2000US-0181749P.
2000US-0195899P.
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2000US-020419P.
2000US-0203630P.
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2000US-021982P.
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2000US-0242333P.
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Pred. No. 7.3e-181;
Mismatches 0;
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Best Local Similarity
Matches 321; Conser
                                                                                                                                                                                                                                                                                                                        The present sequence represents a human G protein-coupled receptor designated TGR7. TGR7 has antiinflammatory, cytostatic, antidiabetic, neuroprotective, vulnerary and antiinfertility activities. TGR7 can be used in the treatment and prevention of central nervous system (CMS) disorders, inflammation, circulatory disorders, cancer, diabetes and infertility. TGR7 can also be used for producing antibodies and antiserums, for researching recombinant receptor expression structure, drug design, for producing probes and polymerase chain reaction (PCR) primers for genetic testing, and for producing transgenic animals
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inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig
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12-MAY-2000; 2000JP-00140435.
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                                                                                               TQRCLSVLFFIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM
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                                                                                                                                                                                                         MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP
                                               VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY
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  WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL
                                                                                TORCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM
                                                                                                                                      FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS
                            VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coupled receptor useful for treating CNS disorders, ion, circulatory disorders, cancer, diabetes and infertility
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                                                                                                                                                                                                                                               Conservative
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Pred. No. 7.3e-181;
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N-PSDB;
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11-JUL-2000; 2000US-0217494P.
26-JAN-2001; 2001EP-00870015.
12-FEB-2001; 2001EP-00870024.
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                                                                                                                                         New G-protein coupled for treating receptor
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)B; AAD27495.
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The present invention runcleotide encoding it.

relates to . GPCR are

a G-protein coupled receptor useful in the manufacture of

(GPCR)

Disclosure;

Page 25; 46pp;

English.

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Best Local
                                                                                                                                                                                                                                       Mouse; human; G-protein coupled receptor; receptor; antipsoriatic; antiulcer; dermatological; vulnerary; gene therapy; skin disease; psoriasis; eczema; acne; wound healing; ulcer; transgenic.
  04-AUG-2000; 2000DE-01038111
                                                                                                                                                 EP1178053-A2
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB08770 standard; protein;
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                                              03-AUG-2001; 2001EP-00118709
                                                                                                  06-FEB-2002
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Pred. No. 7.3e-181;
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Best Local S
Matches 321
                                                 Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
drug development; gustatory; taste; fragrance; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to G-protein coupled receptor polypeptides (I, ABB08769-ABB08772) or their functional variants with antipsoriatic, antiulcer, dermatological and vulnerary activity. (I) and the nucleic acids (II, ABL41224-ABL41227) encoding them, cells containing (II) and antibodies specific for (I) are used for diagnosis, prevention or treatment (including by gene therapy) of skin diseases, especially psoriasis but also eczema, acne, urticaria and pigmentation disorders, wounds and wound healing disorders, particularly ulcers and specifically venous ulcers. The same materials (also transgenic animals containing (II) in the genome) are used for identifying agents for treatment of these discretes.
                                                                                                   Human GPCR polypeptide SEQ ID NO
                                                                                                                                   06-MAR-2003
                                                                                                                                                                   ABP95616;
                                                                                                                                                                                                   ABP95616 standard; protein; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New G protein coupled receptors, useful for diagnosis, treatment and prevention of skin and wound-healing disorders, also related nucleic and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 5; 47pp; German.
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Pred. No. 7.3e-181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database global search for G protein-coupled receptors, proteins encoded genes for studying in vivo signal transduction mechanism identifying targets for drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; SEQ ID NO 42; 97pp + Sequence Listing; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haga T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-2000; 2000JP-00237818.
13-FEB-2001; 2001JP-00034434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 321
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                                                                                                                                                                                                                        TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM
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                                                                                                                                                               VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY
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                       REEPELEGGETPTVGTNEMGA 321
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                                                                   WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL
                                                                                          WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL
                                                                                                                                  VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CC Proteins (I) designated DRG1, DRG2, DRG4, DRG6, DRG7, and DRG8 (see CC ABP96691 to ABP96696) encoded by ACC44767 to ACC44772. (I) can be used CG CABP96691 to ABP96696 encoded by ACC44767 to ACC44772. (I) can be used CG for identifying a compound that modulates pain, by contacting a compound CC with (I), and selecting a compound that binds to the extracellular domain CC or that modulates GPCR activity of the polypeptide. Such compounds that CG modulate the activity of (I) can be used to investigate the role of (I) CC in sensory (e.g. pain) transduction. Biologically active (I) can be used for testing inhibitors and activators of (I) as pain transducers or pain CC inhibitors using in vivo and in vitro expression that measure e.g. CC transcriptional activation of (I), ligand binding, phosphorylation and conductance consisted triphosphate, intracellular second messengers such as cAMP and CC inositol triphosphate, intracellular second messengers such as cAMP and CC release. Such activators and inhibitors identified using (I) can be used to further study sensory transduction and to identify specific pain CC agonists and antagonists. The modulators can be administered directly to the mammalian subject for modulation of pain in vivo
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Best Local Similarity
Matches 321; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel G-protein coupled receptor polypeptide expressed in mammalian sensory neurons of dorsal root ganglia, useful as target for screening for agents that regulate pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-301064/29.
N-PSDB; ACC44770.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G protein-coupled receptor DRG6 protein
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 321 AA;
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                           WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL
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                                                                                          VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY
                                                                                                                                      TORCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM
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WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL
                                                                 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVV
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Pred. No. 7.3e-181;
Mismatches 0;
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RESULT 11
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Best Local
                                                                                                                                                                                                         The invention provides new G-protein coupled receptor (GPCR) polypeptides designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding polynucleotides. The polypeptides can be expressed by standard DNA recombination methodology. The polypeptides are useful for screening or identifying modulators of GPCR or signal transduction. The modulators of signal transduction are useful for treating or preventing TGR-associated disorders, e.g. asthma, multiple sclerosis or kidney disease. The polypeptides are useful as targets for diagnosing or treating e.g. epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia, asymptomatic urinary abnormalities, hypertension, nephrolithiasis, cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute inflammatory dermatoses. The present sequence represents a human TGR2
                                                                                                                                                                                                                                                                                                                                                                                                                                 New G-protein coupled receptor polypeptides designated TGR2, TGR118, TGR164, TGR343 and TGR358, useful as targets for screfor treating or preventing e.g. asthma, multiple sclerosis, tephrolithiasis.
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                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343; TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotropic; anticonvulsant; hypotensive; hepatotropic; dermatological; human; immunosuppressive; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human TGR2 protein.
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FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS
                           FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHBLMKRLMYFAYTVGLSLLTAIS 120
                                                                                                                                                                         321 AA;
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                                                      MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP
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                                                                                                               Score 1661; DB 6;
Pred. No. 7.3e-181;
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screening
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RESULT 12
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                                             useful cancer.
                                                       New nucleic acid encoding a human G-protein coupled receptor (GPCR) known as HGPRBMY31 which is useful for screening or providing GPCR modulators useful for treating diseases involving aberrant GPCR activity, e.g.
                    Claim 5; Fig 2; 219pp; English.
                                                                                                       N-PSDB;
                                                                                                                  WPI; 2003-505194/47.
                                                                                                                                          Mintier GA,
                                                                                                                                                                                        26-NOV-2001;
06-FEB-2002;
                                                                                                                                                                                                                          26-NOV-2002; 2002WO-US038145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGPREMY31; human; G-protein coupled receptor; receptor; cytostatic; gynaecological; analgesic; antiparkinsonian; uropathic; nephrotrophic; neuroprotective; nootropic; immunomodulator; gene therapy.
                                                                                                                                                                                                                                                   05-JUN-2003
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This is the protein sequence of a

splice variant

of human HGPRBMY31,

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CC receptors. HGPRBMY31 constitutively inhibits gene expression through the CC cAMP response element (CRE). HGPRBMY31 (and its splice variant) CC polynuclectides, polypeptides, agonists and antagonists are useful for CC modulating intracellular cAMP levels, modulating cAMP sensitive CC signalling pathways, and modulating the element associated signalling pathways, and modulating CAMP sensitive CC pathways. They can also be used for genetic screening and for the CC treatment of diseases, disorders, conditions or syndromes associated with CC GPCRs, particularly; a reproductive disorder, such as a testicular CC disorder or a cancer; a disorder related to aberrant G-protein coupled CC signalling, particularly pathways that signal through the G alpha i/o CC family of G-proteins; a disorder related to aberrant G-protein coupled CC signalling or GPCR dependent signalling associated with CRE element; an immune disorder; a haematopoletic disorder; a disorder related to aberrant GPCR dependent cAMP CC aberrant G-protein coupled CC groliferative condition of the immune or central nervous system; neural disorder; brain cancer; hypersensitivity disorder; pain disorders; neural disorder related to either a direct or indirect interaction with voltage-gated sodium channels and their beta subunits; disorders related to aberrations or injuries in the cerebellum, including cerebellar ataxias of such as coeliac disease and other diseases associated with this region of the brain, such as Rett syndrome, Parkinson's disease, von Hippel-CC dindau syndrome, familial congenital cerebellar hypoplasia and dysplastic concentral nervous and disorders; urinary incontinence; and overactive bladder (all claimed)
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ID ABWOOSO5
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                                                                                         Human; G-protein coupled receptor; GPCR; infection; neoplastic process; inflammation; myocardial infarction; atherosclerosis; angina pectoris; hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain; diabetes; cancer; virucide; analgesic; cardiant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABW00805 standard; protein; 321
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Pred. No. 7.3e-181;
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sapiens

central nervous system; peripheral nervous G protein coupled receptor; tranquiliser; r

system; neuroleptic;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel G-protein coupled receptors (GPCRs) and the nucleic acids encoding them. The invention is usefur treating viral, bacterial and fungal infections, inflammatory and neoplastic processes, pain, diabettes, hypertension, osteoporosis, angina pectoris, myocardial infarction and atherosclerosis. The presequence is human G-protein coupled receptor (GPCR) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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                                  Human G-protein coupled
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Pred. No. 7.3e-181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myocardial infarction, atherosclerosis.
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Query Match
Best Local S
Matches 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel central or peripheral nervous system function modifier which comprises a G protein coupled receptor. The invention may have tranquiliser, neuroleptic, anticonvulsant, uropathic, hypotensive, vasouropic, neuroprotective, vulnerary or analgesic activities. The invention may be useful as a hypnotic sedative, muscle relaxant, anaesthetic potentiator, for the treatment and prevention of anxiety, cramp, schizophrenia, epilepsy, incontinence, nervous hypertension, miscarriage, premature labour, male impotence, paralysis, spinal vascular damage, multiple sclerosis, spinocerebellar degeneration, after effects of external wounding, surgery, pain, hyperaesthesia and numbness. The present sequence is the amino acid sequence of a human G-protein coupled receptor of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uropathic; hypotensive; vasotropic; neuroprotective; vulnerary; analgesic; hypotic sedative; muscle relaxant; anaesthetic potentiator; anxiety, cramp; schizophrenia; epilepsy; incontinence; nervous hypertension; miscarriage; premature labour; male impotence; cerebrovascular damage; infantile cerebral paralysis; cramp type spinal paralysis; spinal vascular damage; multiple sclerosis; spinocerebellar degeneration; external wounding; surgery; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Central or peripheral nervous system function modifier comprising G protein coupled receptors for example for the treatment of anxiety, cramp, schizophrenia, epilepsy, or incontinence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 4; 143pp; Japanese.
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13-DEC-2002;
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Matches 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to G protein-coupled receptor (GPCR) polypeptides and the polynucleotides encoding them. The GPCR polypeptides are useful for preparing a composition for identifying compounds as receptors, inverse agonists or partial agonists, having potential applicability as inverse agents. This sequence represents a human GPCR polypeptide of the represents a numan GPCR polypeptide of the represents a numan GPCR polypeptide of the respective process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; SEQ ID NO 10; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New G protein-coupled receptor (GPCR), useful for preparing a for identifying compounds as receptors, inverse agonists or pagonists having potential applicability as therapeutic agents.
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(DANG/)
(LOWI/)
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Search completed: November 4, 2004, 11:01:52 Job time : 160 secs	301 RESPELEGGETPTVGTNEMGA 321	301 REEPELEGGETPTVGTNEMGA 321	241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGGRRSHRLPTRSLGTVLQQAL 300

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1: /ggn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /ggn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /ggn2_6/ptodata/1/iaa/ET_COMB.pep:*
5: /ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-254-227A-3
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PCT-US93-08528-76
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US-08-118-270-52
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4 C B B B B B B B B B B B B B B B B B B	8, Appli	7, Appli	2, Appli	274, App	9, Appli	9, Appli	, Appl	64, Ap	-	, Appl	-		48, Appl	254, App	, App	, Appl	, App	٦

# ALIGNMENTS

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APPLICANT: Ahmad, Sultan
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Pacla
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
ITILE OF INVENTION: G Protein-Coupled Receptors from the Rat and Huma
FILE REFERENCE: $1923/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NO.13
SEQ ID NO.13
SEQ ID NO.13
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-227A-13
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5. 6696257
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SLGTVLQQALREEPELEGGE
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                                            PFGILGALIYRMHLNLEVLYCHVYLVCMSL----SSLNSSANPIIYFFVGSFR-QRQNRQ
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APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: C'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Huma
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 322
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SEQ ID NO 11
LENGTH: 322
TYPE: PRT
ORCANISM: Homo sapiens
US-09-254-227A-11
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Best Local Similarity
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CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
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APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: O'Donnell, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
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Banville, Denis
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nilarity 42.4%;
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Pred. No. 7.5e-41;
4; Mismatches 101;
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; TYPE: PRT
; ORGANISM: Homo s
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Best Local S
Matches 135
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 135; Conservat
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ahmad,
APPLICANT: Banvill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Halan
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G PROTEIN-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
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 173
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                                                                                                                                                                                                             1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTC---LCGMAGNSMVIWLLGFRMH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Banville, ve...
                                                            LSLLTAISTQRCLSVLEPIWFKCHRPRHLSAWVCGLLWTLCLLWNGLTSSFCSKFLKFNE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNPFCIYILNLAAADLLFL-----FSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR--CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLV 229
                                   INFLSAVSTDRCLSVIWPIWYRCHRPTHLSAVVCVILWALSLLRSILEWMLCG-FLFSGA 168
                                                                                                       RNAFSIYILNLAAADFLFLSGRLIYSLLSFISI-----PHTISKILYPVMMFSYFAG 109
                                                                                                                                         RNPFCIYILNLAAADLLFL----FSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVG 112
                                                                                                                                                                         PTRSLGTVLQQALREEPELE -- GGETP 312
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                 32.3%; Score 537; DB 4;
41.8%; Pred. No. 1.3e-40;
tive 57; Mismatches 99
                                                                                                                                                                                                                                                                                     DB 4; Length 322;
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; SEQ ID NO 1
; LENGTH: 337
; TYPE: PRT
; ORGANISM: rat
US-09-254-227A-1
                                                                                                                      RESULT 6
US-09-254-227A-3
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US-09-254-227A-1
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                                                                   Sequence 3, Application US/09254227A Patent No. 6696257
GENERAL INFORMATION:
                      APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/99/254,227A
CURRENT FILING DATE: 1999-03-03
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                                                                                                                                                                                                                                                   236 SLTVMVYLICGLELGLYLELLYWEGIHLHYEFCHI--YQVTVLLSCVNSSANEIIYELVG
                                                                                                                                                                                                                                                                                   224 LASVLVFLICSLPLSIYWFVLYWLSLP---PEMQVLCFSLSRLSSSVSSSANPVIYFLVG
                                                                                                                                                                                                                                                                                                                    180 GFLGETHHHLWKNVDFIVTAFLI-FLEMLLFGSSLALLVRILCGS---RKKPLSKLYVTI
                                                                                                                                                                                                                                                                                                                                                  166 KFLKFNEDRCFR-VDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVV
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Ahmad, Sultan
Banville, Denis
Fortin, Yves
Lembo, Paola
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Banville, Denis
Fortin, Yves
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.6%; Score 525; DB 4; Length 337; 40.3%; Pred. No. 1.6e-39; rative 57; Mismatches 95; Indels
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                                                                                                                                             FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 199-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 322
TYPE: PRT
GORGANISM: Homo sapiens
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                                                                  Query Match
Best Local S
Matches 127
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Best Local Similarity 40.3%;
Matches 127; Conservative
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SEQ ID NO 3
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ORGANISM: Homo
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                                                              1 29.6%; Score 492; DB 4; Similarity 40.1%; Pred. No. 1.4e-36; Conservative 57; Mismatches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LORALODTPEVDEGG 305
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APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
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APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and
FILE REFERENCE: 81823/268117
FULL REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1990-03-03
NUMBER OF SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
MDPTVPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
                                                                MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYWFVLYWLSLPPEMQVLCFSLSRLS---SSVSSSANPVIYFLVGSRRSHRLPTRSLGTV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FITIAMLV-FLCVVLCGSSLVLLVRILCGS---RKMPLTRLYVTILLTVLVFLLCGLPFG
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Pred. No. 3.4e-38;
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                                                                                                                                   Indels
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US-08-118-270-76
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                                                                                                           ; MOLECULE TYPE: US-08-118-270-76
                                               Query Match
Best Local Sim:
Matches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                  TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: BROWDY AND NEIMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTED: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/118,270 FILING DATE: 09-SEP-1993
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                                                                                                                                          TOPOLOGY:
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in 26.2%;
Similarity 35.2%;
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Schuster, David I.
Schuster, David I.
VENTION: POLYPETIDES OF G-COUPLED PROTEIN
VENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
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                                                 Score 435.5; DB 1;
Pred. No. 1.6e-31;
6; Mismatches 118;
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PCT-US93-08528-76
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GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF
TITLE OF INVENTION: RECEPTORS, AND
NUMBER OF SEQUENCES: 348
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA: US 07/943,236
APPLICATION NUMBER: US 07/943,236
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                    Query Match
Best Local 9
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE: |
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ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acid
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                  / Match
Local Similarity 35.2%;
les 106; Conservative 56
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                                                         29 VLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIXI--LNLAAADLLFLFSMASTLSLE
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                                                                                                                                                                                                                                                                                                                                                                                amino acid
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   VTNYIFLLLCLCGLVGNGLVLWFFGFSIKRTFFSIYIYFLHIASADGIYLFSKAVIALLN
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                  298 amino acids
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VENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
VENTION: RECEPTORS, AND COMPOSITIONS AND MI
EQUENCES: 348
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                                                                                                                         Score 435.5; DB 5
Pred. No. 1.6e-31;
6; Mismatches 118
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RESULT 10
5320941-2
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                                                             RESULT 11
US-08-118-270-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA SEQUENCES ENCODING MAS ONHCOGENE, POLYPETIDES ENCODED THEREFROM AND DIAGNOSTIC AND OTHER METHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASED
             Sequence 52, Application Patent No. 5508384 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 06-JUN-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Young, Dallan; Wigler, Michael H.; Fasano
APPLICANT: Murphy,
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                                                                                                                                                                                                                          228 LVFLICSLPLSIYWFVL--YWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSH 285
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                                                                                                                                                           RIPTRSIGTVLQQALREE 303
                                                                                                                                                                                         IIFLIFAMRMRLLYLLYYEYWSTFGN-----LHDISLLFSTINSSANNFIYFFVGSSKKK 289
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                                                                                                                              RF-KQSLKVVTTRAFKDE 306
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Randall B
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31.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 397.5; DB 6; Pred. No. 4.9e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117;
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RESULT 12

PCT-US93-08528-52
; Sequence 52, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
. NUMBER OF ADDRESS:
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 21.9%; Score 364.5; DB 1; Similarity 32.4%; Pred. No. 3.9e-25; 97; Conservative 57; Mismatches 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDYALD-----YELSSGHYYTIVTLSVTFLFGYNTGLYLLTAISVERCLSVLYP
                                                                                                                                                                                                                                                 YWSTFGN-----LHHISLLFSTINSSANPFIYFFVGSSKKKRF-KESLKVVLTRAFKDE
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POLYPEPTIDES OF G-COUPLED PROTEIN
RECEPTORS, AND COMPOSITIONS AND METHODS
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US-09-170-496D-246
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Cc
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
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                                                                                                                                                                        Sequence 246, Application US/09170496D Patent No. 6555339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
COERRATING SYSTEM: PC-DOS/M-100
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LENGTH: 282 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
RBFERENCE/DOCKET NUMBER: MURPHY=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 419 Sever CITY: Washington
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                                                                                                                                                                                                                                                                                                             YWSTFGN----LHHISLLFSTINSSANPFIYFFVGSSKKKRF-KESLKVVLTRAFKDE 263
                                                                                                                                                                                                                                                                                                                                                                                                                    MGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR----CFRVDMVQAALI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STLSLETQPLVNTTDKVHELMKRLMY-----FAYTVGLSLLTAISTQRCLSVLFP
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419 Seventh Street, N.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.9%; Score 364.5; DB 5; 32.4%; Pred. No. 3.9e-25; tive 57; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/943,236
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                                                                                               Constitutively Activated Human G
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                                                                                                     Protein
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; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo s
US-09-170-496D-270
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US-09-170-496D-270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 270
LENGTH: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 270, Application Patent No. 6555339
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                 Query Match 14.6%; Score 243; DB 4; Length 356; Best Local Similarity 24.4%; Pred. No. 4.7e-14; Matches 86; Conservative 62; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.7%; Score 244; DB 4; Length 356; Best Local Similarity 24.4%; Pred. No. 3.8e-14; Matches 86; Conservative 62; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Behan, Dominic P. APPLICANT: Chalmers, Derek T. APPLICANT: Liaw, Chen W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 6555339-Endogenous, TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: AREN-0040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo
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                           118 AISTQRCLSVLEPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR--- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 ALGCVNSSLNPFLYVFVGRDFQEKF-FQSLTSALARAFGEEEFLSSCPRGNAP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 LSSSVSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREEPELEG---GETP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 AISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR--- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CIYILNLAAADLLELESMASTLSLETQPLVNTTDKVHELMKRL----MYFAYTVGLSLLT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
                                                                                                                                        62 CIYILNLAAADLLELESMASTLSLETQPLVNTTDKVHELMKRL----MYFAYTVGLSLLT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 TVCFFHLALAD----FMLSLSLPIAMYYIVSRQWLLGEWACKLYITFVFLSYFASNCLLV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPF 61
                                                                                                                                                                                                                                      2 NQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPF 61
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                                                                                                                                                                                        SRKMNSSGCLSEEVGSLRPLTV----VILSA----SIVVGVLGNGLVLWMTVFRMARTVS 77
FISVDRCISVLYPVWALNHRTVQRASWLAFGVWL-----LAAALCSAHLKFRTTRKWN 186
                                                                                             TVCFFHLALAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWVHANRPARLLLVLVSAFFIFW----SPFNVVLLVHLWRRVMLKEIYHPRM-LLILQASF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QW--RRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYWLSL-----PPEMQVLCFSLSR 262
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                                                                                             -FMLSLSLPIAMYYIVSRQWLLGEWACKLYITFVFLSYFASNCLLV 133
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194 216	148 LLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDMVQAALIMGVLTPVM	유 성
158		Дb
147	LSVLFPIWFKCHRPRHLSAWV-CG	Ş
99	9 LVGVLGNALVVWVTAFEAKRTINAIWFLNLAVADFLSCLALPILFTSIVQH	뭥
98	FLFSMASTLSLETQPLVNTTDKVH	Ş
12;	Query Match 14.5%; Score 240.5; DB 2; Length 350; Best Local Similarity 26.8%; Pred. No. 7.7e-14; Matches 84; Conservative 55; Mismatches 117; Indels 57; Gaps	3 8 0
	MOLECULE TYPE: 08-458-970A-9	us-
	STRANDEDNESS: TOPOLOGY: linear	
	350 amino nino acid	٠. ٠.
	INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:	~· ·· ·
	201- 201-99	٠. ٠.
	MATION	٠. ٠.
	33,073	. ~
	ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G.	٠. ٠.
	AFFILING DATE: 16 AUG 1994	·· ·
	199	
1	APPLICATION NUMBER: US/08/458,970A	٠
	ECI	. ~.
	S-DC	٠. ٠.
	MEDIUM TYPE: 3.5 INCH DISKETTE	·· ··
	ZIP: 07068	. ~-
	STATE: NEW JERSEY COUNTRY: USA	٠. ٠.
	HAND	
	CHI, STEWART & OLSTEI	
	CARRILA BYRNE BAIN G	. ~.
	TITLE OF INVENTION: C5a Receptor NUMBER OF SEQUENCES: 11	٠. ٠.
	APPLICANT: LI, ET AL.	
	nt No. 5861272	ייי.
	SSULT 15 3-08-458-970A-9 Sequence 9. Application US/08458970A	RES
	303 ALGCVNSSLNPFLYVFVGRDFQEKF-FQSLTSALARAFGEEEFLSSCPRGNAP 354	DЬ
	SSANPVIYFLVGSRRSHRLPTRSLGTVLQ	Ş
302	247 GWVHANRPKRLLLVLVSAFFIFWSPFNVVLLVHLWRRVMLKEIYHPRM-LLILQASF	В
262	CSLPLSIYWFVLYWLSLPPEMQVLCFSLSR	Ś
246	WIEGVVEGHIIGTIGHFLLGFLGPLAIIGTCAHLIRAKLLRE	DЬ
210	175CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQ	Ş

Search completed: November 4, 2004, 11:06:38
Job time: 40 secs

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Minimum
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re greater than or equal to the score of the result being po
is derived by analysis of the total score distribution.
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1661
1 MNQTLNSSGTVESALN
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1: pir1:*
2: pir2:*
3: pir3:*
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MNQTLNSSGTVESALNYSRG.....
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S51001
A39485
A465209
C42009
S27357
A37963
JC64520
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A41796
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          somatostatin recep
somatostatin recep
G protein-coupled
somatostatin recep
G protein-coupled
somatostatin recep
G protein-coupled
probable G protein
G protein-coupled
                                                                                                                                                                                                                                                             complement C5a ana complement C5a ana G protein-coupled N-formyl peptide r probable chemoattr N-formyl peptide c
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somatostatin recep
G protein-coupled
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## ALIGNMENTS

G protein-coupled receptor RTA - rat C,Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A35639
R;Ross, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Harcus, D Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990
A;Title: RTA, a candidate G protein-coupled receptor: cloning, sequencing, A;Reference number: A35639; MUID:90222168; PMID:2109324
A;Accession: A35639; MUID:90222168; PMID:2109324

C.M.; Adam, N.; Harcus, D.R.;

and tissue

di: ×

Lynch,

PID:g206810

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A;Molecule type: mRNA
A;Residues: 1-343 <ROS>
A;Cross-references: UNIPROT:P23749; GB:M35297; NID:g206809; PIDN:AAA42087.1;
C;Superfamily: mas transforming protein
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein
F;4/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Best Local Similarity
Matches 121; Conserv
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                                                         IVSVPLVSSIYLGIDWFLFWVFQIPAPFPEY----VTDLCICINSSAKPIVYFLAGRD
                                                                                       SATALTICSTPISIAMEATAMTST5--- bEWOATCESTSETSSASSAWEAIAETAGSE
                                                                                                                                         L--KENEDRCFRYDMVQAALIMGVLTPVMTLSSLTLFVMVRRSSQQWRRQPTRLFVVVLA
                                                                                                                                                                                    WFFGFSIKRTPFSIYFLHLASADGIYLFSKAVIALLNMGTF-LGSFPDYVRRVSRIVGLC
                            RSHRLPTRSLGTVLQQALRE--EPELEGGETPTVGTNEM 319
                                                                                                                          LGHBASGTACLNMDISLGILLFFLFCPLMVLPCLALILHVECRARR-RORSAKLNHVVLA
KSQRL-WEPLRVVFQRALRDGAEPGDAASSTPNTVTMEM
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Pred. No. 9e-
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RESULT TVRTAS

transforming protein mas - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 09-Jul-2004

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A;Map position: 6q24-6q27
(;Superiamily: mas transforming protein
C;Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming prote
P;31-61/Domain: transmembrane #status predicted <TM1>
F;66-97/Domain: transmembrane #status predicted <TM2>
F;165-135/Domain: transmembrane #status predicted <TM3>
F;150-172/Domain: transmembrane #status predicted <TM4>
F;150-172/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                              transforming protein mas - human C,Species: Homo sapiens (man) C,Date: 04-Dec-1986 #sequence_revision C,Accession: A01375.
R,Young, D.; Waitches, G.: Birchmeier
F;105-135/Domain: transmembrane #status predicted <TM3>F;150-172/Domain: transmembrane #status predicted <TM4>F;186-214/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                 A; Cross-references: GDB:120166; OMIM:165180
                                                                                                                                                                                                                             C;Genetics:
A;Gene: GDB:MAS1
                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: P04201; GB:M13150;
                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-325 < YOU>
                                                                                                                                                                                                                                                                                                                                                                   A; Title: Isolation and characterization of A; Reference number: A01375; MUID: 86218084;
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R;Young, D.; O'Neill, K.; Jessell, T.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 5339-5342, 1988
A;Title: Characterization of the rat mas oncogene and its high-level expression
A;Reference number: A31816; MUID:88276953; PMID:2455902
A;Accession: A31816...
                                                                                                                                                                                                                                                                                                                                              A; Accession: A01375
                                                                                                                                                                                                                                                                                                                                                                                                                       R;Young, D.; Waitches, G.; Birchmeier, Cell 45, 711-719, 1986
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C;Keywords: G protein-coupled receptor; transforming protein; transmembrane
F;31-47/Domain: transmembrane #status predicted <TM2>
F;72-88/Domain: transmembrane #status predicted <TM2>
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A; Residues: 1-324 < YOU>
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Best Local :
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-Dec-1986 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                     a new cellular oncogene PMID:3708691
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A;Gene: mas
C;Superfamil
C;Keywords:
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NyAlternate names: mas proto-oncogene protein; probable G protein-coupled receptor
C;Species: Mus musculus (house mouse)
C;Pate: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S51001; 148647; S29619
R;Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.
FBBS Lett. 357, 27-32, 1995
A;Title: Expression of the mouse and rat mas proto-oncogene in the brain and periph
A;Reference number: S51001; MUID:95094925; PMID:8001672
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                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-87,'I',89-324 <RES>
A; Cross-references: EMBL:X67735;
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Expression of the mouse and rat mas proto-oncogene A;Reference number: I48647; MUID:95094925; PMID:8001672 A;Accession: I48647
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P30554; EMBL:X67735 R;Metzger, R.; Bader, M.; Ludwig, T.; Berberich, FEBS Lett. 357, 27-32, 1995
                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-324 < MET>
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                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                       Superfamily: mas transforming protein
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Best Local Similarity
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                                                                                                                                                                                                                G protein-coupled receptor; proto-oncogene; transmembrane
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WILGERMHRNPECIXILNIAAADLLELESMASTISLETQPLVNTTDKV--HELMKRLMY- 106
                                           MDQSNMTSLAEEKAMNTSSRNASLGSSHPPIPIVHWVIMSISPL-
                                                                                  MNQTLNSSGTVESALNYSR-----GST-----VHTAYLVLSSLAMFTCLCGMAGNSMVI 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RF-KESLKVVLTRAFKDE
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                                                                                                                                Conservative
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                                                                                                                           26.3%; Score 437; DB 2;
33.8%; Pred. No. 2.5e-30;
tive 61; Mismatches 112
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                                                                                                                                                                                                                                                                                                        NID:g53011; PIDN:CAA47964.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303
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Pred. No. 1.9e-30;
"'ematches 114;
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                                                                                                                                                                       Length 324
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                                         -GFVENGILL
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transforming protein (mrg) - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A39485
R;Monnot, C; Weber, V; Stinnakre, J.; Bihoreau, C; Teutsch, B.; Corvol, P.; Clauser,
Mol. Endocrinol. 5, 1477-1487, 1991
A;Title: Cloning and functional characterization of a novel mas-related gene, modulating
A;Reference number: A39485; MUID:92130997; PMID:1723144
A;Reference number: A39485; MUID:92130997; PMID:1723144
A;Accession: A39485
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <MON>
A;Residues: 1-378 <MON>
A;Cross-references: UNIPRCT:P35410; GB:S78653; NID:g244209; PIDN:AAB21255.1; PID:g244210
C;Keywords: G protein-coupled receptor; transmembrane protein
complement C5a anaphylatoxin receptor -
;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision
C;Accession: A46525
R;Gerard, C.; Bao, L.; Orozco, O.; Pear
                                                                                        RESULT
A46525
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Best Local Similarity
Matches 110; Conserv
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                                                                                                                                                           NKKAA 350
                                                                                                                                                                                                                                                CFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREBPELEGGETPTVGT 316
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                                                                                                                                                                                            NEMGA 321
                                                                                                                                                                                                                            TSYLISLFLIINSSANPIIYFFVGSLRKKRL-KESLRVILQRALADKPE-
                                                                                                                                                                                                                                                                                               SSLTLLIRFLCCSQQ-
                                                                                                                                                                                                                                                                                                                             SSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLFLSIYWFVLYWLSLPPEMQVL
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 Pearson,
                                                                                                                                                                                                                                                                                                                                                                                                 -----CSKFLKFNEDRCFRVDMVQAALIMGVLTPVMTL
                             10-Sep-1999 #text_change 10-Sep-1999
                                                                     mouse
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Kunz,
D.; Gerard, N.P.
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C;Superfamily: vertebrate rhodopsin
C;Reywords: chemotaxis; G protein-coupled receptor; glycop:
F;1-37/Domain: extracellular #status predicted <TX1>
F;38-61/Domain: transmembrane #status predicted <TM1>
F;62-71/Domain: intracellular #status predicted <TM1>
F;62-71/Domain: extracellular #status predicted <TM2>
F;72-94/Domain: transmembrane #status predicted <TM2>
F;95-110/Domain: extracellular #status predicted <TM2>
F;111-132/Domain: transmembrane #status predicted <TM2>
F;111-132/Domain: transmembrane #status predicted <TM2>
F;133-149/Domain: transmembrane #status predicted <TM3>
F;109-289/Domain: transmembrane #status predicted <TM3>
F;209-249/Domain: transmembrane #status predicted <TM5>
F;209-249/Domain: transmembrane #status predicted <TM5>
F;244-265/Domain: transmembrane #status predicted <TM5>
F;244-265/Domain: transmembrane #status predicted <TM5>
F;266-284/Domain: transmembrane #status predicted <TM5>
F;
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A;Note: sequence extracted from NCBI backbone (NCBIP:116075)
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A;Accession: A46525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 149, 2600-2606, 1992
A;Title: Structural diversity in the extracellular faces of peptidergic G-protein-coupled A;Reference number: A46525; MUID:93017861; PMID:1401897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: mediates the inflammatory and chemotactic responses of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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    314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
    RSLPSITRNALSEDSVGRDSKTFTPSTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AALIIYSVVF---LVGVPGNALVVWVTAFEPDGPSNAIWFLNLAVADLLSCLAM-----
                                                                                                                                                                                                                               IYWFVLYWLSLPP-----EMQVLCFSLSRLSSSVSSANPVIYFLVGSRRSHRLPT
                                                                                                                                                                                                                                                                                                                                                                                                --ALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTR---LFVVVLASVLVFLICSLPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKVRGTGLAWMACGVAWVLALLLTIPSFVYREAYKDFYSEHTVCGINYGGGSFPKEKAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETQPLVNTTDKVHB-----LMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIYILNLAAADLLFLFSMASTLSL
                                                                       RSLGTVLQQALREEPELEGGETPTVGTNE 318
                                                                                                                                                        VTGVMIAW--LPPSSPTLKRVEKLNSLCVSLAYINCCV---
                                                                                                                                                                                                                                                                                                                ILREMVGFVLPLLTLNICYTFLLLR----TWSRKATRSTKTLKVVMAVVICFFIFWLPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PVLFTTVLNHNYWYFDATACIVLPSLILLNMYASILLLATISADRFLLVFKPIW--C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 263.5;
; Pred. No. 2.8e
54; Mismatches
342
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                                                                                                                                                   -NPIIYVMAGQGFHGRL-L
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                                                                                                                                                                                                                                    289
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FMLP-related receptor 2 - human NyAlternate names: FMLP-related CySpecies: Homo sapiens (man) CyDate: 30-Sep-1993 #sequence_re CyAccession: C42009
RiBao, L.; Gerard, N.P.; Eddy Jr., R.L.; Sho
genomics 13, 437-440, 1992
A;Title: Mapping of genes for the human C5a
A;Reference number: A42009; MUID:92307681; P
                                                                                 N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard,
                                                                                                                                     #sequence_revision 30-Sep-1993
     receptor (C5AR),
PMID:1612600
                                                                                                                                  #text_change
```

receptor I; probable chemotactic receptor

09-Jul-2004

human

FMLP receptor

(FPR),

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F;39-62/Domain: transmembrane #status predicted <TM1>
F;63-72/Domain: intracellular #status predicted <IN1>
F;73-95/Domain: transmembrane #status predicted <TM2>
F;73-95/Domain: extracellular #status predicted <EX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
S27357
                                                                                   F;112-133/Domain: transmembrane #status predicted <TM3>
F;134-150/Domain: intracellular #status predicted <TM2>
F;151-175/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M.
Biochem. J. 288, 911-917, 1992
A;Title: Cloning and functional expression of the canine anaphylatoxin A;Reference number: S27357; MUID:93111969; PMID:1472004
A;Accession: S27357
      F;230-244/Domain:
                            F;176-208/Domain:
F;209-229/Domain:
                                                                                                                                                                                                                                                                                                   F;1-38/Domain: extracellular #status predicted
                                                                                                                                                                                                                                                                                                                                      C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P30992; EMBL:X65860; NID:g878; PIDN:CAA46690.1; PID:g879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement C5a anaphylatoxin receptor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S27357
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A;Map position: 19q13.3-19q13.4
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P25089; GB:M76673; NID:g182668; PID:g182669
C;Comment: This fMet-Leu-Phe receptor homolog, whose ligand is not yet known,
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-352 < PER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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A;Molecule type: DNA
A;Residues: 1-353 <BAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                             ;Superfamily: vertebrate rhodopsin;Keywords: chemotaxis; G protein-co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 RHLS-----AWVCGLL-----WTLCLLMNGLTSSFCSKFLKFNEDRCFR-----VD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 HTAYLVLSSLAM-FTCLCGMAGNSMVIWLLGFRMHRNPFCIYILNLAAADLLFL----FS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - IRSLPTSLERALTEVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLPLSIYWFVL-YWLS---LPPEMQVLCFSLSRLSSSV--SSSANPVIYFLVGSRRSHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSLAKRVMTGLWIFTIVLTLENFIFWTTISTTNG--DTYCIFNFAFWGDTAVERLNVFIT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFPYELIGILMAVWLKEMLLNGKYKIILVLINPTSSLAFFNSCLNPILYVFMGRNFQERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAKVFLILHFIIGFTVPMSIITVCYGIIAAKIHRNHMIKSSRPLRVFAAVVAS---FFIC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVQAALIM----GVLTP--VMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVSVAMREKWPFASFLCKLVHVMIDINLF---VSVYLITIIALDRCICVLHPAWAQNHRT 138
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: extracellular
: transmembrane
: intracellular
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                                                                                                                                                                                                                                                                                                   protein-coupled receptor; glycoprotein; inflammation; polymoz;
lar #status predicted <EX1>
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28.6%; Pred. No. 9.2e-15;
#status predicted <EX3>
#status predicted <TM5>
#status predicted <IN3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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A;Residues: 1-350 <BOUY
A;Cross-references: UNIPROT:P21730; GB:J05327; NID:g179699; PIDN:AAA62831.1; PID:g179700
R;Gerard, N.P.; Gerard, C.
Nature 349, 614-617, 1991
Nature 349, 614-617, 1991
A;Tittle: The Chemotactic receptor for human C5a anaphylatoxin.
A;Reference number: 813646; MUID:91156029; PMID:1847994
A;Accession: S13646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
A37963
A; Introns:
A; Note: the
                         A;Map position: 19q13.3-19q13.4
A;Introns: 1/3
                                                                                                                                                                                                                                                                                       Biochemistry 32, 1243-1250, 1993
A,Title: Human chemotaxis receptor genes cluster at 19q13.3-13.4.
A,Reference number: I52417; MUID:93192225; PMID:8383526
                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X58674; NID:g29568; PIDN:CAB37830.1; PID:g4467832 R;Gerard, N.P.; Bao, L.; Xiao-Ping, H.; Eddy, R.L. Biochemistry 32, 1243-1250, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement C5a anaphylatoxin receptor - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: A37963; S13646; T52417; S30518
R;Boulay, F.; Mery, L.; Tardif, M.; Brouchon, L.; Vignais, P.
Biochemistry 30, 2993-2999, 1991
                                                                             A;Gene: GDB:C5R1; C5A; C5AR
A;Cross-references: GDB:128856;
                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                   A; Accession: I52417
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-350 < GER >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Expression cloning of a receptor for C5a anaphylatoxin A; Reference number: A37963; MUID:91175748; PMID:2007135
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F;310-352/Domain:
F;5/Binding site:
                                                                                                                                                                                        A;Residues:
                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
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F;267-285/Domain:
                                                                                                                                                              ;Cross-references:
                                                                                                                                    Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 LAAQGFHSRFLKSLPAR-----LRQVLAEESVGRDSKSITLST 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 SADRFVLVFNPIWCQNYRGPQLAWAACSVAWAVALLLTVPSFIFRGVHTEYFPFWMTCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 WFLNLAVADLLSCLALPILFSSIVQQGYWFFGNAACRI---LPSLILLLMYASILLLTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 YILNLAAADLLFLFSMASTLSLETQ----PLVNTTDKVHELMKRLMYFAYTVGLSLLTAI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
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  list of introns may be incomplete
                                                                                                                                                                                     1-3 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLM-----NGLTSSFCSKFLKFNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYSGVGVLVERGVAILRLLMGFLGPLVILSICYTFLLIR----TWSRKATRSTKTLKVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRCFRVDMVQAA----LIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTR---LFVVVL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLDPNIFVDESLNTPKLSVPDMIALVIFVMVF----LVGVPGNFLVVWVTGFEVRRTINAI
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extracellular #status predicted <EX4>
transmembrane #status predicted <TM7>
intracellular #status predicted <TM4>
carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                              GB:S56556; GB:S56557; NID:g298577; NID:g298578
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Pred. No. 2.2e-13;
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257

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C;Keywords: Chemotaxis; G protein-coupled receptor; glycoprotein; inf: F;1-37/Domain: extracellular #status predicted <TM1>F;3-61/Domain: transmembrane #status predicted <TM1>F;3-61/Domain: transmembrane #status predicted <TM1>F;2-71/Domain: intracellular #status predicted <TM1>F;72-94/Domain: extracellular #status predicted <TM2>F;72-94/Domain: transmembrane #status predicted <TM3>F;111-113/Domain: transmembrane #status predicted <TM3>F;133-149/Domain: intracellular #status predicted <TM3>F;133-149/Domain: intracellular #status predicted <TM3>F;150-174/Domain: extracellular #status predicted <TM3>F;175-206/Domain: extracellular #status predicted <TM5>F;207-227/Domain: transmembrane #status predicted <TM5>F;208-342/Domain: transmembrane #status predicted <TM6>F;243-242/Domain: transmembrane #status predicted <TM6>F;243-264/Domain: transmembrane #status predicted <TM6>F;265-283/Domain: extracellular #status predicted <TM4>F;308-350/Domain: intracellular #status predicted <TM7>F;308-350/Domain: intracellular #status predicted <TM7>F;308-350/Domain: intracellular #status predicted <TM7>F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                              G protein-coupled receptor DEZ - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: JC5498
R;Methner, A.; Hermey, G.; Schinke, B.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 233, 336-342, 1997
A;Title: A novel G protein-coupled receptor with homology to neuropeptide and chemoattra A;Reference number: JC5498; MUID:97289630; PMID:9144535
A;Contents: Brain
A;Accession: JC5498
A;Molecule type: mRNA
A;Residues: 1-371 cMET'>
A;Cross-references: UNIPROT:P97468; GB:U79525; NID:g1732346; PIDN:AAB53789.1; PID:g17323
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
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C;Superfamily: C;Keywords: cher
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Best Local S
Matches 84
    Query Match
Best Local S
Matches 82
                        Local Similarity
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    82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PELEGGETPTVGT
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13.8%; Score 230; DB 2; ilarity 21.5%; Pred. No. 2.3e-12; Conservative 62; Mismatches 148
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ilarity 26.8%;
Conservative 5
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5; Mismatches
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Pred. No. 2.
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hes 117;
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    148;
                                            Length 371;
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  Indels
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  11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-formyl peptide receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 18-Unn-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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A, Note: sequence extracted from NCBI backbone (NCBIP:124908)
C, Superfamily: vertebrate rhodopsin
C, Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-352 <YEl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A46520
R;Ye, R.D.; Quehenberger, O.; Thomas, K.M.; Navarro,
J. Immunol. 150, 1383-1394, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The rabbit neutrophil N-formyl peptide receptor. A;Reference number: A46520; MUID:93163563; PMID:8432984 A;Accession: A46520
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l Similarity 26.7%;
94; Conservative 5
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                                                                                                                                                                                                                                                                          LAD----FSFTSTLPFFIVTKALGGHWPFGWFLCK----FVFTIVDINLFGSVFLIALIA
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                                                                                                                                                                                  LDRCICVLHPVWAQNHRNVSLAKKVIVGPWICALLLTLPVIIRVTTLSHPRAPGKWACTF
                                                                                                                                                                                                                                                                                                                      AADLLFLFSMASTLS--LETQPLVNTTDKVHELMKRLMYFAYTV-----GLSLLTAIS
                                            PTRLFVVVLASVLVFLICSLPLSIYWFVL-----YWLSLPPEMQVLCFSLSRLSSSVSS
                                                                                        DWSPWTEDPAEKLKVAISMFMVRGIIRFIIGFSTPMSIVAVCYGLIATKIHRQGLIKSSR
PLRVLSFVVAS---FLLCWSPYQIAALIATVRIRBLLLGMGKDLRIV-LDVTSFVAFFNS
                                                                                                                                      KFLKFNEDRCFRVD-----MVQAAL--IMGVLTP--VMTLSSLTLFVWVRRSSQQWRRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSK 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDSGIYDD--EYSDGFGYFVDLEEASPWEAKVAPVFLVV--IYSLVCFLGLLGNGLVIVI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTIVFKLORNRLAKNKKP---FKIIITIIITFFLCWCPYHTLYLLELHHTAVPSSVFSLG 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 228; DB 2;
Pred. No. 3.3e-12;
88; Mismatches 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 352
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240

180 165

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SANPVIYFLVGSRRSHRLPTRSLGTVLQQALRESPELEGGETPTVGTNEMGA

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F;39-62/Domain: transmembrane #status predicted <TM1>
F;74-94/Domain: transmembrane #status predicted <TM2>
F;112-135/Domain: transmembrane #status predicted <TM2>
F;156-177/Domain: transmembrane #status predicted <TM4>
F;206-237/Domain: transmembrane #status predicted <TM4>
F;206-237/Domain: transmembrane #status predicted <TM5>
F;209-280/Domain: transmembrane #status predicted <TM6>
F;302-317/Domain: transmembrane #status predicted <TM7>
F;7,190/Binding site: carbohydrate (Asn) (covalent) #status
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R;Owman, C.; Lolait, S.J.; Santen, S.; Olde, B.
Biochem. Biophys. Res. Commun. 241, 390-394, 1997
A;Title: Molecular cloning and tissue distribution of cDNA
A;Reference number: JC5796; MUID:98086361; PMID:9425281
A;Accession: JC5796
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1998 #sequence_revision 13
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                                                                                                                                            A.49542
N-formyl peptide chemotactic receptor -
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 2
C;Accession: A49542
J. Biol. Chem. 268, 25395-25401, 1993
                                   R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 268, 25395-25401, 1993
A;Title: Species aubtype variants of the N-formyl peptide chemotactic receptor revea
A;Title: Species aubtype variants of the N-formyl peptide chemotactic receptor revea
A;Title: Species aubtype variants of the N-formyl peptide chemotactic receptor revea
A;Title: Species audition of the N-formyl peptide chemotactic receptor revea
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A;Residues: 1-371 <OWM>
A;Accession: A49542
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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| 79; | Conser
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Pred. No. 2.3e-11;
5; Mismatches 140;
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A;Cross-references: UNIPROT:P46090; GB:S74702; NID:g786483; PIDN:AAB32978.1; C;Superfamily: vertebrate rhodopsin C;Reywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester b F;74-94/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM2>
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JC2492
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A;Residues: 1-364 <GAO>
A;Cross-references: UNIPROT:P33766; GB:L22181; NID:g347396; PIDN:AAA16110.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein-coupled receptor 1 - rat
N;Alternate names: GPR-1
C;Species: Rattus norvegicus (Norway rat)
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C;Superfamily: vertebrate rhodopsin
C;Keywords: Chemotaxis; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 205, 1952-1958, 1994
A;Title: Mapping studies of two G protein-coupled receptor
A;Reference number: JC2492; MUID:95110347; PMID:7811287
A;Accession: JC2492
                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 16-Mar-1995 #sequence_revision
C;Accession: JC2492
R;Marchese, A.; Cheng, R.; Lee, M.C.; I
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                                                                    7,155-175/Jomain: transmembrane #status predicted <TM4>
7,209-229/Domain: transmembrane #status predicted <TM5>
7,246-266/Jomain: transmembrane #status predicted <TM6>
7,246-266/Jomain: transmembrane #status predicted <TM6>
7,295-306/Domain: transmembrane #status predicted <TM7>
7,295-306/Domain: transmembrane #status predicted <TM7>
7,295-306/Jomain: transmembrane #status predicted <TM7>
7,14,273/Binding site: phosphate (Thr) (covalent) #status predicted
7,150,231/Binding site: palmitate (Cys) (covalent) #status predicted
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                  12.5%;
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Score 208; DB 2;
Pred. No. 1.8e-10;
B; Mismatches 140
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      38;
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A;Accession: JG1258
A;Status: nucleic acid sequence not shown
A;Nolecule type: mRNA
A;Residues: 1-351 cPER>
A;Status: nucleic acid sequence not shown
A;Nolecule type: mRNA
A;Residues: 1-351 cPER>
A;Cross-references: EMBL:X63819; NID:g31460; PID:g31461
A;Experimental source: bone marrow mRNA
R;Ye, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.; Cochrane, C.G.
Biochem. Biophys. Res. Commun. 184, 582-589, 1992
A;Title: Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide recep
A;Reference number: JQ1521; MUID:92246937; PMID:1374236
A;Accession: JQ1521
A;Molecule type: mRNA
A;Residues: 1-351 cyE2>
A;Cross-references: GB:M88107; NID:g189862; PID:g189863
A;Experimental source: granulocytes
A;Note: formyl peptide-stimulated calcium mobilization comparable to that of the formyl peptide-stimulated calcium mobilization comparable to that of the formyl peptide-stimulated calcium mobilization comparable to that of the formyl peptide-stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formyl peptide stimulated calcium mobilization comparable to that of the formy
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A;Note: sequence extracted from NCBI backbone
R;Nomura, H; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-351 < MUR>
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Gene 118, 303-304, 1992
A;Title: Cloning of a cDNA encoding a receptor related to the formyl peptide receptor A;Reference number: CC1258; MUID:92380523; PMID:1511907
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NyAlternate names: FMLP receptor homolog FPR2; formyl peptide receptor like-1; probable C;Species: Homo sapiens (man)

C;Date: 30-Gep-1993 #sequence revision 14-Jul-1995 #text change 09-Jul-2004

C;Accession: B42009; JC1258; JQ1521; A42492; 154751; S21581

R;Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.

Genomics 13, 437-440, 1992

Genomics 13, 437-440, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VHWISLLLYALAF---VLGIPGNAIVIWFMGFKWKKTVTTLWFLNLAIADFIFVLFLPLY
                                                                      PIDN:AAA52473.1;
ne (NCBIN:94159, )
                                                                  ; PID:g182742
NCBIP:94160)
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F;59-83/Domain: transmembrane #status predicted <TM1>
F;59-83/Domain: transmembrane #status predicted <TM2>
F;100-121/Domain: transmembrane #status predicted <TM3>
F;145-169/Domain: transmembrane #status predicted <TM4>
F;206-226/Domain: transmembrane #status predicted <TM5>
F;206-226/Domain: transmembrane #status predicted <TM5-
F;208-2007/Domain: transmembrane #status predicted <TM6>
F;282-307/Domain: transmembrane #status predicted <TM6>
F;282-307/Domain: transmembrane #status predicted <TM6>
F;448:Inding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leu:
A; Reference number: I54751; MUID:94092629; PMID:7505609
A; Accession: I54751
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: I-351 < RES>
A; Cross-references: GB.10922; NID:g219864; PIDN:BAA01720.1; PID:g219865
C; Comment: This G-protein coupled receptor, homologous to the N-formyl peptid:
differentiated myeloid cells and is probably a chemotactic receptor for some of Genetics:
A; Gene: GDB:PPRL1
A; Cross-references: GDB:127554; OMIM:136538
A; Map position: 19413.3-19413.4
A; Map position: 19413.3-19413.4
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C;Keywords: chemotaxis; G protein-coupled receptor;
F;27-53/Domain: transmembrane #static prodicted -mar
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V--SSSANPVIYFLYGSRRSHRLPTRSLGTVLQQALREEPELEGGETPTVGTNEMGA 321
                                                           SRPLRVLTAVVAS ---FFICWFPFQLVALLGTVWLK---
                                                                                                                                                                                                                      KFN-----EDRC-FRVDMVQA----ALIMGVLTP--VMTLSSLTLFVWVRRSSQQWR
                                                                                                                                                                                                                                                                                                                           RCLSVLFPIWFKCHRPRHLS-----AWVCGLLWTLCLLM-----NGLTSSFCSKFL 168
                                                                                                             ROPTRLFVVVLASVLVFLICSLPLSIYWFV-LYWLSLPPEM-----
                                                                                                                                                                                                                                                                        RCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNG--DTYCT---
                                                                                                                                                                   - FNFASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKS
                                                                                                                                                                                                                                                                                                                                                                                ----FSFTATL----PFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALD 122
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25.8%; Pred. No. 2.4e-10;
tive 56; Mismatches 126
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